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 Gerritsen, Mary E.
 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, J. Christopher
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 Hillan, Kenneth J
 Kljavin, Ivar J.
 Kuo, Sophia S.
 Napier, Mary A.
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 Roy, Margaret Ann
 Shelton, David L.
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Val	Glu	Met	Leu	Ala	Ser	Tyr	Gly	Leu	Ala	Tyr	Ser	Leu	Met	Lys
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	50	55	60
Phe Phe Thr Gly Pro Met Ser Asp Phe Lys Asn Val Gly Leu Val	65	70	75
Phe Val Asn Ser Lys Arg Asp Arg Thr Lys Ala Val Leu Cys Met	80	85	90
Val Val Ala Gly Ala Ile Ala Ala Val Phe His Thr Leu Ile Ala	95	100	105
Tyr Ser Asp Leu Gly Tyr Tyr Ile Ile Asn Lys Leu His His Val	110	115	120
Asp Glu Ser Val Gly Ser Lys Thr Arg Arg Ala Phe Leu Tyr Leu	125	130	135
Ala Ala Phe Pro Phe Met Asp Ala Met Ala Trp Thr His Ala Gly	140	145	150
Ile Leu Leu Lys His Lys Tyr Ser Phe Leu Val Gly Cys Ala Ser	155	160	165
Ile Ser Asp Val Ile Ala Gln Val Val Phe Val Ala Ile Leu Leu	170	175	180
His Ser His Leu Glu Cys Arg Glu Pro Leu Leu Ile Pro Ile Leu	185	190	195
Ser Leu Tyr Met Gly Ala Leu Val Arg Cys Thr Thr Leu Cys Leu	200	205	210
Gly Tyr Tyr Lys Asn Ile His Asp Ile Ile Pro Asp Arg Ser Gly	215	220	225
Pro Glu Leu Gly Gly Asp Ala Thr Ile Arg Lys Met Leu Ser Phe	230	235	240
Trp Trp Pro Leu Ala Leu Ile Leu Ala Thr Gln Arg Ile Ser Arg	245	250	255
Pro Ile Val Asn Leu Phe Val Ser Arg Asp Leu Gly Gly Ser Ser	260	265	270
Ala Ala Thr Glu Ala Val Ala Ile Leu Thr Ala Thr Tyr Pro Val	275	280	285
Gly His Met Pro Tyr Gly Trp Leu Thr Glu Ile Arg Ala Val Tyr	290	295	300
Pro Ala Phe Asp Lys Asn Asn Pro Ser Asn Lys Leu Val Ser Thr	305	310	315
Ser Asn Thr Val Thr Ala Ala His Ile Lys Lys Phe Thr Phe Val	320	325	330
Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe Trp Thr	335	340	345

Pro Asn Val Ser	Glu Lys Ile Leu Ile	Asp Ile Ile Gly Val	Asp
	350	355	360
Phe Ala Phe Ala	Glu Leu Cys Val Val	Pro Leu Arg Ile Phe	Ser
	365	370	375
Phe Phe Pro Val	Pro Val Thr Val Arg	Ala His Leu Thr Gly	Trp
	380	385	390
Leu Met Thr Leu	Lys Lys Thr Phe Val	Leu Ala Pro Ser Ser	Val
	395	400	405
Leu Arg Ile Ile	Val Leu Ile Ala Ser	Leu Val Val Leu Pro	Tyr
	410	415	420
Leu Gly Val His	Gly Ala Thr Leu Gly	Val Gly Ser Leu Leu	Ala
	425	430	435
Gly Phe Val Gly	Glu Ser Thr Met Val	Ala Ile Ala Ala Cys	Tyr
	440	445	450
Val Tyr Arg Lys	Gln Lys Lys Lys Met	Glu Asn Glu Ser Ala	Thr
	455	460	465
Glu Gly Glu Asp	Ser Ala Met Thr Asp	Met Pro Pro Thr Glu	Glu
	470	475	480
Val Thr Asp Ile	Val Glu Met Arg Glu	Glu Asn Glu	
	485	490	

<210> 8
 <211> 535
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> unsure
 <222> 33, 66, 96, 387
 <223> unknown base

<400> 8
 cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50
 tgagctttctg gtgccntttg gctctaattc tggccacaca gagaancagt 100
 cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
 agccacagag gcagtgggoga ttttgacagc cacataccct gtgggtcaca 200
 tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250
 aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300
 ggcccacatc aagaagttca ccttcgtctg catggctctg tcaactcacgc 350
 tctgtttcgt gatgttttgg acaccaacg tgtctgngaa aatcttgata 400
 gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450

gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcatctca 500

ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9

<211> 434

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361

<223> unknown base

<400> 9

tgacggaatc ccgggctggg taccctgggt tngacaagat aaacccccag 50

caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100

agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150

gttttggaca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200

tggantttgc ctttgcagaa ntttgnngtg ttcctttgcg gattttctcc 250

tttttcccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350

ttgtcctnat ngccagcctt gtggctctac cctacctggg ggtgcacggg 400

gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10

<211> 154

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 49, 68, 83, 90, 98, 119

<223> unknown base

<400> 10

tattcccagt tccggtcacg gggagggcgc atntcaccgg gtggctgang 50

acactgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100

cgtctcctac gccagcctng tggctctacc ctacctgggg gtgcacgggtg 150

agac 154

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gctctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcattctttc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttcgcca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 17

tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18

<211> 1901

<212> DNA

<213> Homo sapiens

<400> 18

gccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50

gcctgcctgg gagcctgctc cctgtcagc tgcgcgtcct gcctctgcgg 100

ctctgcccc tgcattcctgt gcagctgtg ccccgccagc cgcaactcca 150

ccgtgagccg cctcatcttc acgttcttcc tcttctggg ggtgctggtg 200

tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250

ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300

tcgactgtgg ctccctgctt ggctaccgag ctgtctaccg catgtgcttc 350

gccacggcgg ctttcttctt cttctttttt accctgctca tgctctgcgt 400

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ttaagttcct gatcctggtg ggcctcaccg tgggtgcctt ctacatccct 500

gacggctcct tcaccaacat ctggttctac ttcggcgtcg tgggctcctt 550

cctcttcac ctcattcagc tgggtgctgct catcgacttt gcgcactcct 600

ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650

tacgcaggcc tcttcttctt cactctcctc ttctacttgc tgtcgatcgc 700

ggccgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750

agggcaaggt cttcatcagc ctcaacctca ccttctgtgt ctgcgtgtcc 800

atcgctgctg tcctgccccaa ggtccaggac gccagccca actcgggtct 850

gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctgggtcag 900

ccctatccag tatccctgaa cagaaatgca acccccattt gccaaaccag 950

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 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800
 tggtcacgtc ccccagggga cctgcccc ttctggact tcgtgcctta 1850
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900

a 1901

<210> 19

<211> 457

<212> PRT

<213> Homo sapiens

<400> 19

Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser
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Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro
 20 25 30

Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe
 35 40 45

Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly
 50 55 60

Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly	65	70	75
Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser	80	85	90
Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	95	100	105
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	110	115	120
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	125	130	135
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr	140	145	150
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val	155	160	165
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	170	175	180
Asp	Phe	Ala	His	Ser	Trp	Asn	Gln	Arg	Trp	Leu	Gly	Lys	Ala	Glu	185	190	195
Glu	Cys	Asp	Ser	Arg	Ala	Trp	Tyr	Ala	Gly	Leu	Phe	Phe	Phe	Thr	200	205	210
Leu	Leu	Phe	Tyr	Leu	Leu	Ser	Ile	Ala	Ala	Val	Ala	Leu	Met	Phe	215	220	225
Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val	Phe	230	235	240
Ile	Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala	245	250	255
Val	Leu	Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu	260	265	270
Gln	Ala	Ser	Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser	275	280	285
Ala	Leu	Ser	Ser	Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro	290	295	300
Thr	Gln	Leu	Gly	Asn	Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr	305	310	315
Glu	Thr	Gln	Trp	Trp	Asp	Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile	320	325	330
Phe	Leu	Leu	Cys	Thr	Leu	Phe	Ile	Ser	Leu	Arg	Ser	Ser	Asp	His	335	340	345
Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met			

	350		355		360
Leu Asp Ala Thr	Gln Gln Gln Gln Gln	Gln Val Ala Ala Cys	Glu		
	365		370		375
Gly Arg Ala Phe	Asp Asn Glu Gln Asp	Gly Val Thr Tyr Ser	Tyr		
	380		385		390
Ser Phe Phe His	Phe Cys Leu Val Leu	Ala Ser Leu His Val	Met		
	395		400		405
Met Thr Leu Thr	Asn Trp Tyr Lys Pro	Gly Glu Thr Arg Lys	Met		
	410		415		420
Ile Ser Thr Trp	Thr Ala Val Trp Val	Lys Ile Cys Ala Ser	Trp		
	425		430		435
Ala Gly Leu Leu	Leu Tyr Leu Trp Thr	Leu Val Ala Pro Leu	Leu		
	440		445		450
Leu Arg Asn Arg	Asp Phe Ser				
	455				

<210> 20
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 20
 gccgcctcat cttcacgttc ttcc 24

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 21
 tcatccagct ggtgctgctc 20

<210> 22
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 22
 cttcttccac ttctgcctgg 20

<210> 23
 <211> 18

09978197 101501
105107 287660

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
cctgggcaaa aatgcaac 18

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggaatgta gaaggcaccc acgg 24

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
tggcacagat cttcacccac acgg 24

<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50
ttaacctggg tcaaatgcac ggattctcac ctcgtaacagt tacgctctcc 100
cgcggcacgt ccgcgaggac ttgaagtccg gagcgctcaa gtttgtccgt 150
aggctcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250

actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300
 cccagagccc tattaccggg aatctggatg ggaccgcctc cgggagctgt 350
 ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400
 aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450
 agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500
 ttatcataa ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550
 cgaggcttca ttcgttatgg ctggcgctgg ggttggagaa ctgcagtgtt 600
 tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650
 aagatgcctt aagccatttt gtaattgcag gagctgtcac ggggaagtctt 700
 tttaggataa acgtaggcct gcgtggcctg gtggctggtg gcataattgg 750
 agccttgctg ggcactcctg taggaggcct gctgatggca tttcagaagt 800
 acgctggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850
 catgagctaa aactggaaga gtggaaaggc agactacaag ttactgagca 900
 cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950
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 gtactctcac ttacttata cttaaattta aatacatact tatgtttgta 1250
 ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300
 aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350
 t 1351

<210> 28
 <211> 285
 <212> PRT
 <213> Homo sapiens

<400> 28
 Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala
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 Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala
 20 25 30

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	35	40	45
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	50	55	60
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	65	70	75
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	80	85	90
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	95	100	105
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	110	115	120
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	125	130	135
Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	140	145	150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	155	160	165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	170	175	180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	185	190	195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	200	205	210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	215	220	225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	230	235	240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	245	250	255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	260	265	270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	275	280	285

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

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ctattacccg gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100
 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300
 ttcgttcgat gctggcgccg aacc 324

<210> 30
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 262, 330, 371
 <223> unknown base

<400> 30
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 accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100
 gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150
 gcggcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
 gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250
 cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300
 gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350
 agagccaggc agaaatttat nataacc 377

<210> 31
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 31
 tcgtacagtt acgctctccc 20

<210> 32
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 32
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 34
gctaataatct gtaagacggc agctacagca ggcattcattg 40

<210> 35
<211> 1819
<212> DNA
<213> Homo sapiens

<400> 35
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ccaccacgt ctgcgttgcg gccccgcctg ggccaggccc caaaggcaag 100
gacaaagcag ctgtcaggga acctcgcgcg gagtcgaatt tacgtgcagc 150
tgccggcaac cacagggtcc aagatggttt gcggggggtt cgcgtgttcc 200
aagaactgcc tgtgcgcctt caacctgctt tacaccttg ttagtctgct 250
gctaattgga attgctgcgt ggggcattgg ctccgggctg atttccagtc 300
tccgagtggc cggcgtgggc attgcagtgg gcattcttctt gttcctgatt 350
gcttttagtgg gtctgattgg agctgtaaaa catcatcagg tgttgcatt 400
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cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750
 agaaagaccc ccgcgcgaat cctagtgcac tcctttgatg agaaaacaag 800
 gaagatttcc tttcgtatta tgatcttggt cactttctgt aattttctgt 850
 taagctccat ttgccagttt aaggaaggaa acactatctg gaaaagtacc 900
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 ggtggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050
 cctttcttag catttttacc tgcagaaaaa ctttgtatgg taccactgtg 1100
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 agcactgtgc tgtgtagata gttcctactg gaaaaagagt ggaaatttat 1200
 taaaatcaga aagtatgaga tcctgttatg ttaagggaaa tccaaattcc 1250
 caattttttt tgggtctttt aggaaagatt gttgtggtaa aaagtgttag 1300
 tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350
 ctagaaaatg ttatgtctta ggaaattgtg gtttaatttt tgacttttac 1400
 aggtaagtgc aaaggagaag tggtttcatg aaatgttcta atgtataata 1450
 acatttacct tcagcctcca tcagaatgga acgagttttg agtaatcagg 1500
 aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550
 aagactgcat ttttaaacaa gttagtatta atgctgtggc ccacgtagca 1600
 aaaagatatt tgattatctt aaaaattgtt aaataccgtt ttcattgaaat 1650
 ttctcagtat tgtaacagca acttgtcaaa cctaagcata tttgaatatg 1700
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750
 gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800
 taaaagaaag taatggaag 1819

<210> 36
 <211> 204
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Cys Leu Cys Ala
 1 5 10 15
 Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile
 20 25 30

Ala Ala Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val
35 40 45

Val Gly Val Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala
50 55 60

Leu Val Gly Leu Ile Gly Ala Val Lys His His Gln Val Leu Leu
65 70 75

Phe Phe Tyr Met Ile Ile Leu Leu Leu Val Phe Ile Val Gln Phe
80 85 90

Ser Val Ser Cys Ala Cys Leu Ala Leu Asn Gln Glu Gln Gln Gly
95 100 105

Gln Leu Leu Glu Val Gly Trp Asn Asn Thr Ala Ser Ala Arg Asn
110 115 120

Asp Ile Gln Arg Asn Leu Asn Cys Cys Gly Phe Arg Ser Val Asn
125 130 135

Pro Asn Asp Thr Cys Leu Ala Ser Cys Val Lys Ser Asp His Ser
140 145 150

Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu Tyr Ala Gly Glu Val
155 160 165

Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe Ser Phe Thr Glu
170 175 180

Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn Gln Lys Asp
185 190 195

Pro Arg Ala Asn Pro Ser Ala Phe Leu
200

<210> 37
<211> 390
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336
<223> unknown base

<400> 37
tgattggagc tgtaaaaaan tottcaggtg ttgtnatttt tttatatgat 50
tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttggt 100
tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150
aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200
gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250
gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300

gaggttttga gatttgttgg tggcattggc ctgttnttca gttttacaga 350
 gatcctgggt gtttggctga cctacagata caggaaccag 390

<210> 38
 <211> 566
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 27
 <223> unknown base

<400> 38
 aatcccaaat tccccaat ttttggncctt tttagggaaa gatgtgttgt 50
 ggtaaaaagt gttagtataa aaatgataat ttacttgttag tcttttatga 100
 ttacaccaat gtattctaga atagttagt cttaggaaat tgtggtttta 150
 tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200
 tctaattgtat aataacat t acccttcagcc tcccatcaga atggaacgag 250
 ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
 taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgag 350
 ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
 ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450
 gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500
 ggaggaaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550
 gttgtgcccc acttgc 566

<210> 39
 <211> 264
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 84-85, 206
 <223> unknown base

<400> 39
 atgattattc tggttacttgt atttattgtt cagttttatg gtatcttgag 50
 cttgttttagc ccctgaaacc aggagcaaca gggnnacagc tcttgagggt 100
 tggttggcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150
 aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200

09978187.101501

tggtngctg tggtaaaagt gaccactcgt gctcgccatg tgctccaatc 250

ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

acccacgtct gcgttgctgc c 21

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 41

gagaatatgc tggagagg 18

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 42

aggaatgcac taggattcgc gcgg 24

<210> 43

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 43

ggcccccag gcaaggacaa agcagctgtc agggaaacctc cgccg 45

<210> 44

<211> 2061

<212> DNA

<213> Homo sapiens

<400> 44

cagtcacat gaagctgggc tgtgtcctca tggcctgggc cctctacctt 50

tcccttggtg tgctctgggt ggcccagatg ctactggctg ccagttttga 100

09978187 101501

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 tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250
 cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300
 gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350
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 accccaagca ggaagcccca tgaccctgag ttgtcagaca aagttgcccc 600
 tgcagaggtc agctgcccgc ctctcttct cttctacaa ggatggaagg 650
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 agaagatcac tccgggtcat actggtgtga ggcagccact gaggacaacc 750
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 ccccatcttc tgaggatcca ggcttttctt ctctctggg gatgccagat 950
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 ctctctgtcc tgcacatatg cataagtact tttacaagtt gtcccagtgt 1200
 tttgttagaa taatgtagtt aggtgagtg aaataaattt atataaagt 1250
 agaattagag tttagctata attgtgtatt ctctcttaac acaacagaat 1300
 tctgctgtct agatcaggaa ttctatctg ttatatcgac cagaatgttg 1350
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 ggggcaattt tgccccccag aggacattgg gcaatgtttg gagacatttt 1450
 ggtcattata cttgggggggt tgggggatgg tgggatgtgt gtctactggc 1500
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gagtttgaga aaccccagcc taatgaaacc ctaggtgttg ggctctggaa 1650
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cagagccctc atgattagga ttagtgccct tatttaaaaa ggccccagag 1900
agctaactca cccttccacc atatgaggac gtggcaagaa gatgacatgt 1950
atgagaacca aaaaacagct gtcgccaac accgactctg tcgttgccct 2000
gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050
tttagccta a 2061

<210> 45
<211> 359
<212> PRT
<213> Homo sapiens

<400> 45
Met Lys Leu Gly Cys Val Leu Met Ala Trp Ala Leu Tyr Leu Ser
1 5 10 15
Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe
20 25 30
Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser
35 40 45
Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe
50 55 60
Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val
65 70 75
Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe
80 85 90
Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp
95 100 105
Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly
110 115 120
Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys
125 130 135
Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro
140 145 150

Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	155	160	165
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	170	175	180
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	185	190	195
Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
tttccagcgc caattctc 18

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtcctcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

<400> 51
cccacgcgtc cgcacacgcg tccgccacg ggtccgccca cgcgtccggg 50
ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150
gcacctaaac gtggacactt atggccgtcc catcctggaa gtgccagaga 200
gtgtaacagg accttggaac ggggatgtga atcttcctg cacctatgac 250
cccctgcaag gctacacca agtcttggtg aagtggctgg tacaacgtgg 300
ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350

agcaggcaaa gtaccagggc cgcttgcacg tgagccacaa ggttccagga 400
 gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450
 cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500
 ataagattac tgagctccgt gtccagaaac tctctgtctc caagcccaca 550
 gtgacaactg gcagcgggta tggcttcacg gtgccccagg gaatgaggat 600
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 accttactct tcaagcctgc ggtgatagcc gactcaggct cctatttctg 750
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ctttgccctg gaatttgcca gatgcatctc aagtaagcca gctgctggat 1850
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 tctaaatacc agagggaaga tgcccatagc actaggactt ggtcatcatg 1950
 cctacagaca ctattcaact ttggcatctt gccaccagaa gacccgaggg 2000
 aggctcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050
 ctttcttcag ggccagacag cttttaattg aaattgttat ttcacaggcc 2100
 agggttcagt tctgctcctc cactataagt ctaatgttct gactctctcc 2150
 tggtgctcaa taaatatcta atcataacag c 2181

<210> 52
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val
 1 5 10 15
 Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr
 20 25 30
 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro
 35 40 45
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg
 50 55 60
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp
 65 70 75
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His
 80 85 90
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met
 95 100 105
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro
 110 115 120
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val
 125 130 135
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly
 140 145 150
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys
 155 160 165
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln
 170 175 180

Gln Thr Asn Asn	Gln Glu Pro Ile Lys	Val Ala Thr Leu Ser Thr	185	190	195
Leu Leu Phe Lys	Pro Ala Val Ile Ala Asp	Ser Gly Ser Tyr Phe	200	205	210
Cys Thr Ala Lys	Gly Gln Val Gly Ser	Glu Gln His Ser Asp Ile	215	220	225
Val Lys Phe Val	Val Lys Asp Ser Ser	Lys Leu Leu Lys Thr Lys	230	235	240
Thr Glu Ala Pro	Thr Thr Met Thr Tyr	Pro Leu Lys Ala Thr Ser	245	250	255
Thr Val Lys Gln	Ser Trp Asp Trp Thr	Thr Asp Met Asp Gly Tyr	260	265	270
Leu Gly Glu Thr	Ser Ala Gly Pro Gly	Lys Ser Leu Pro Val Phe	275	280	285
Ala Ile Ile Leu	Ile Ile Ser Leu Cys	Cys Met Val Val Phe Thr	290	295	300
Met Ala Tyr Ile	Met Leu Cys Arg Lys	Thr Ser Gln Gln Glu His	305	310	315
Val Tyr Glu Ala	Ala Arg		320		

<210> 53
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 53
 tatccctcca attgagcacc ctgg 24

<210> 54
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 54
 gtcggaagac atccaacaa g 21

<210> 55
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

gcgccgggag cccatctgcc cccaggggca cggggcgcg ggcgggtcc 50

cgccccggcac atggtgtcag ccacctcgcg cgcaccccca ggccgcgcgc 100

ccagctcgcc cgaggtccgt cggaggcgcc cggccgcccc ggagccaagc 150

agcaactgag cggggaagcg cccgcgtccg gggatcgga tgtccctcct 200

ccttctctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250

ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300

caactggggc ttccagaaaa agacactctg gatattgaat ggctgtcac 350

cgataatgaa gggaaccaa aagtggatgat cacttactcc agtcgtcatg 400

tctacaataa cttgactgag gaacagaagg gccgagtggc ctttgcttcc 450

aatttctctg caggagatgc ctccttgag attgaacctc tgaagcccag 500

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 aaccaccctg gacgagttct gctgcagaat cttaccatgt cctactctgg 800
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 ccagaggtga gaggttctga accaaagaaa gtccaccatg ctaactctgac 1250
 caaagcagaa accacaccca gcatgatccc cagccagagc agagccttcc 1300
 aaacggtctg aattacaatg gacttgactc ccacgctttc ctaggagtca 1350
 gggctcttgg actcttctcg tcattggagc tcaagtcacc agccacacaa 1400
 ccagatgaga ggtcatctaa gtagcagtga gcattgcacg gaacagattc 1450
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 gattcatctg taaaaaggca tcttattgtg ccttttagacc agagtaaggg 1550
 aaagcaggag tccaaatcta tttgttgacc aggacctgtg gtgagaagg 1600
 tggggaaagg tgagggtgaat atacctaaaa cttttaatgt gggatatttt 1650
 gtatcagtgc tttgattcac aattttcaag aggaaatggg atgctgtttg 1700
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 cagtcaagca gaaccacag ccttattaca cctgtctaca ccatgtactg 1800
 agctaaccac ttctaagaaa ctccaaaaaa ggaaacatgt gtcttctatt 1850
 ctgacttaac ttcatttgtc ataaggtttg gatattaatt tcaaggggag 1900
 ttgaaatagt gggagatgga gaagagtga tgagtttctc cactctata 1950
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 aatttgtgac aaaggattgt gaagagcttt ccatcttcat gatgttatga 2050
 ggattgttga caaacattag aaatatataa tggagcaatt gtggatttcc 2100

cctcaaatca gatgcctcta aggactttcc tgctagatat ttctggaagg 2150
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 <212> PRT
 <213> Homo sapiens

<400> 59
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 35 40 45
 Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln
 50 55 60
 Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu
 65 70 75
 Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu
 80 85 90
 Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp
 95 100 105
 Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val
 110 115 120
 Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro
 125 130 135
 Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr
 140 145 150
 Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr
 155 160 165
 Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro
 170 175 180

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Pro	Lys	Ser	Arg	Ile	Asp	Tyr	Asn	His	Pro	Gly	Arg	Val	Leu	Leu
				185					190					195
Gln	Asn	Leu	Thr	Met	Ser	Tyr	Ser	Gly	Leu	Tyr	Gln	Cys	Thr	Ala
				200					205					210
Gly	Asn	Glu	Ala	Gly	Lys	Glu	Ser	Cys	Val	Val	Arg	Val	Thr	Val
				215					220					225
Gln	Tyr	Val	Gln	Ser	Ile	Gly	Met	Val	Ala	Gly	Ala	Val	Thr	Gly
				230					235					240
Ile	Val	Ala	Gly	Ala	Leu	Leu	Ile	Phe	Leu	Leu	Val	Trp	Leu	Leu
				245					250					255
Ile	Arg	Arg	Lys	Asp	Lys	Glu	Arg	Tyr	Glu	Glu	Glu	Glu	Arg	Pro
				260					265					270
Asn	Glu	Ile	Arg	Glu	Asp	Ala	Glu	Ala	Pro	Lys	Ala	Arg	Leu	Val
				275					280					285
Lys	Pro	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Arg	Ser	Ser	Arg	Ser	Gly
				290					295					300
Ser	Ser	Ser	Thr	Arg	Ser	Thr	Ala	Asn	Ser	Ala	Ser	Arg	Ser	Gln
				305					310					315
Arg	Thr	Leu	Ser	Thr	Asp	Ala	Ala	Pro	Gln	Pro	Gly	Leu	Ala	Thr
				320					325					330
Gln	Ala	Tyr	Ser	Leu	Val	Gly	Pro	Glu	Val	Arg	Gly	Ser	Glu	Pro
				335					340					345
Lys	Lys	Val	His	His	Ala	Asn	Leu	Thr	Lys	Ala	Glu	Thr	Thr	Pro
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

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<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61
actaggctgt atgcctgggt gggc 24

<210> 62
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 63
<211> 3534
<212> DNA
<213> Homo sapiens

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 attaataaac attaggtggt tggttaaaaa aaaa 3534

<210> 64
 <211> 655
 <212> PRT
 <213> Homo sapiens

<400> 64
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 Arg Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu
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Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	
				35					40					45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	
				50					55					60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	
				65					70					75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	
				80					85					90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	
				95					100					105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	
				110					115					120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	
				125					130					135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	
				140					145					150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	
				155					160					165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	
				170					175					180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	
				185					190					195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	
				200					205					210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	
				215					220					225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	
				230					235					240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	
				245					250					255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	
				260					265					270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	
				275					280					285	
Glu	Asp	Val	Asn	Lys	Thr	Leu	Pro	Asn	Leu	Gln	Val	Val	Asn	His	
				290					295					300	
Gln	Gln	Gly	Pro	His	His	Arg	His	Ile	Leu	Lys	Leu	Leu	Pro	Ser	
				305					310					315	
Met	Glu	Ala	Thr	Gly	Gly	Glu	Lys	Ser	Ser	Thr	Pro	Ile	Lys	Gly	

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				320					325					330
Pro	Lys	Arg	Gly	His	Pro	Arg	Gln	Asn	Leu	His	Lys	His	Phe	Asp
				335					340					345
Ile	Asn	Glu	His	Leu	Pro	Trp	Met	Ile	Val	Leu	Phe	Leu	Leu	Leu
				350					355					360
Val	Leu	Val	Val	Ile	Val	Val	Cys	Ser	Ile	Arg	Lys	Ser	Ser	Arg
				365					370					375
Thr	Leu	Lys	Lys	Gly	Pro	Arg	Gln	Asp	Pro	Ser	Ala	Ile	Val	Glu
				380					385					390
Lys	Ala	Gly	Leu	Lys	Lys	Ser	Met	Thr	Pro	Thr	Gln	Asn	Arg	Glu
				395					400					405
Lys	Trp	Ile	Tyr	Tyr	Cys	Asn	Gly	His	Gly	Ile	Asp	Ile	Leu	Lys
				410					415					420
Leu	Val	Ala	Ala	Gln	Val	Gly	Ser	Gln	Trp	Lys	Asp	Ile	Tyr	Gln
				425					430					435
Phe	Leu	Cys	Asn	Ala	Ser	Glu	Arg	Glu	Val	Ala	Ala	Phe	Ser	Asn
				440					445					450
Gly	Tyr	Thr	Ala	Asp	His	Glu	Arg	Ala	Tyr	Ala	Ala	Leu	Gln	His
				455					460					465
Trp	Thr	Ile	Arg	Gly	Pro	Glu	Ala	Ser	Leu	Ala	Gln	Leu	Ile	Ser
				470					475					480
Ala	Leu	Arg	Gln	His	Arg	Arg	Asn	Asp	Val	Val	Glu	Lys	Ile	Arg
				485					490					495
Gly	Leu	Met	Glu	Asp	Thr	Thr	Gln	Leu	Glu	Thr	Asp	Lys	Leu	Ala
				500					505					510
Leu	Pro	Met	Ser	Pro	Ser	Pro	Leu	Ser	Pro	Ser	Pro	Ile	Pro	Ser
				515					520					525
Pro	Asn	Ala	Lys	Leu	Glu	Asn	Ser	Ala	Leu	Leu	Thr	Val	Glu	Pro
				530					535					540
Ser	Pro	Gln	Asp	Lys	Asn	Lys	Gly	Phe	Phe	Val	Asp	Glu	Ser	Glu
				545					550					555
Pro	Leu	Leu	Arg	Cys	Asp	Ser	Thr	Ser	Ser	Gly	Ser	Ser	Ala	Leu
				560					565					570
Ser	Arg	Asn	Gly	Ser	Phe	Ile	Thr	Lys	Glu	Lys	Lys	Asp	Thr	Val
				575					580					585
Leu	Arg	Gln	Val	Arg	Leu	Asp	Pro	Cys	Asp	Leu	Gln	Pro	Ile	Phe
				590					595					600
Asp	Asp	Met	Leu	His	Phe	Leu	Asn	Pro	Glu	Glu	Leu	Arg	Val	Ile
				605					610					615

Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu
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Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu Leu Asp
635 640 645

Ser Val Tyr Ser His Leu Pro Asp Leu Leu
650 655

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
gtagcagtgc acatggggtg ttgg 24

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
accgcacatc ctcaagtctct gtcc 24

<210> 67
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 67
acgatgatcg cgggctccct tctcctgctt ggattcotta gcaccaccac 50

<210> 68
<211> 2412
<212> DNA
<213> Homo sapiens

<400> 68
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<210> 69
 <211> 453
 <212> PRT
 <213> Homo sapiens

<400> 69
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 Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro
 35 40 45
 Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile
 50 55 60
 Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly
 65 70 75
 Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala
 80 85 90
 Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr
 95 100 105
 Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe

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Thr Ala Ala Ser	Trp Lys Thr Met Cys	Ser Asp Asp Trp Lys	Gly
	125	130	135
His Tyr Ala Asn	Val Ala Cys Ala Gln	Leu Gly Phe Pro Ser	Tyr
	140	145	150
Val Ser Ser Asp	Asn Leu Arg Val Ser	Ser Leu Glu Gly Gln	Phe
	155	160	165
Arg Glu Glu Phe	Val Ser Ile Asp His	Leu Leu Pro Asp Asp	Lys
	170	175	180
Val Thr Ala Leu	His His Ser Val Tyr	Val Arg Glu Gly Cys	Ala
	185	190	195
Ser Gly His Val	Val Thr Leu Gln Cys	Thr Ala Cys Gly His	Arg
	200	205	210
Arg Gly Tyr Ser	Ser Arg Ile Val Gly	Gly Asn Met Ser Leu	Leu
	215	220	225
Ser Gln Trp Pro	Trp Gln Ala Ser Leu	Gln Phe Gln Gly Tyr	His
	230	235	240
Leu Cys Gly Gly	Ser Val Ile Thr Pro	Leu Trp Ile Ile Thr	Ala
	245	250	255
Ala His Cys Val	Tyr Asp Leu Tyr Leu	Pro Lys Ser Trp Thr	Ile
	260	265	270
Gln Val Gly Leu	Val Ser Leu Leu Asp	Asn Pro Ala Pro Ser	His
	275	280	285
Leu Val Glu Lys	Ile Val Tyr His Ser	Lys Tyr Lys Pro Lys	Arg
	290	295	300
Leu Gly Asn Asp	Ile Ala Leu Met Lys	Leu Ala Gly Pro Leu	Thr
	305	310	315
Phe Asn Glu Met	Ile Gln Pro Val Cys	Leu Pro Asn Ser Glu	Glu
	320	325	330
Asn Phe Pro Asp	Gly Lys Val Cys Trp	Thr Ser Gly Trp Gly	Ala
	335	340	345
Thr Glu Asp Gly	Gly Asp Ala Ser Pro	Val Leu Asn His Ala	Ala
	350	355	360
Val Pro Leu Ile	Ser Asn Lys Ile Cys	Asn His Arg Asp Val	Tyr
	365	370	375
Gly Gly Ile Ile	Ser Pro Ser Met Leu	Cys Ala Gly Tyr Leu	Thr
	380	385	390
Gly Gly Val Asp	Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu	Val
	395	400	405

Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe
 410 415 420

Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg
 425 430 435

Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp
 440 445 450

Leu Lys Thr

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

tgacatcgcc cttatgaagc tggc 24

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

tacacgtccc tgtggttgca gatc 24

<210> 72

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 72

cgttcaatgc agaaatgac cagcctgtgt gcctgcccac ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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gcacgcacac acacgggggg aaactttttt aaaaatgaaa ggctagaaga 150

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp
 50 55 60
 Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu
 65 70 75
 Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile
 80 85 90
 Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp
 95 100 105
 Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly
 110 115 120
 His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys
 125 130 135
 Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val
 140 145 150
 Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro
 155 160 165
 Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His
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 Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser
 185 190 195
 Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr
 200 205 210

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Lys Tyr Val Glu	Leu Val Ile Val Ala	Asp Asn Arg Glu Phe	Gln
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Arg Gln Gly Lys	Asp Leu Glu Lys Val	Lys Gln Arg Leu Ile	Glu
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Ile Ala Asn His	Val Asp Lys Phe Tyr	Arg Pro Leu Asn Ile	Arg
245	250		255
Ile Val Leu Val	Gly Val Glu Val Trp	Asn Asp Met Asp Lys	Cys
260	265		270
Ser Val Ser Gln	Asp Pro Phe Thr Ser	Leu His Glu Phe Leu	Asp
275	280		285
Trp Arg Lys Met	Lys Leu Leu Pro Arg	Lys Ser His Asp Asn	Ala
290	295		300
Gln Leu Val Ser	Gly Val Tyr Phe Gln	Gly Thr Thr Ile Gly	Met
305	310		315
Ala Pro Ile Met	Ser Met Cys Thr Ala	Asp Gln Ser Gly Gly	Ile
320	325		330
Val Met Asp His	Ser Asp Asn Pro Leu	Gly Ala Ala Val Thr	Leu
335	340		345
Ala His Glu Leu	Gly His Asn Phe Gly	Met Asn His Asp Thr	Leu
350	355		360
Asp Arg Gly Cys	Ser Cys Gln Met Ala	Val Glu Lys Gly Gly	Cys
365	370		375
Ile Met Asn Ala	Ser Thr Gly Tyr Pro	Phe Pro Met Val Phe	Ser
380	385		390
Ser Cys Ser Arg	Lys Asp Leu Glu Thr	Ser Leu Glu Lys Gly	Met
395	400		405
Gly Val Cys Leu	Phe Asn Leu Pro Glu	Val Arg Glu Ser Phe	Gly
410	415		420
Gly Gln Lys Cys	Gly Asn Arg Phe Val	Glu Glu Gly Glu Glu	Cys
425	430		435
Asp Cys Gly Glu	Pro Glu Glu Cys Met	Asn Arg Cys Cys Asn	Ala
440	445		450
Thr Thr Cys Thr	Leu Lys Pro Asp Ala	Val Cys Ala His Gly	Leu
455	460		465
Cys Cys Glu Asp	Cys Gln Leu Lys Pro	Ala Gly Thr Ala Cys	Arg
470	475		480
Asp Ser Ser Asn	Ser Cys Asp Leu Pro	Glu Phe Cys Thr Gly	Ala
485	490		495
Ser Pro His Cys	Pro Ala Asn Val Tyr	Leu His Asp Gly His	Ser

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Cys Gln Asp Val	Asp Gly Tyr Cys Tyr	Asn Gly Ile Cys Gln Thr			
	515		520		525
His Glu Gln Gln	Cys Val Thr Leu Trp	Gly Pro Gly Ala Lys Pro			
	530		535		540
Ala Pro Gly Ile	Cys Phe Glu Arg Val	Asn Ser Ala Gly Asp Pro			
	545		550		555
Tyr Gly Asn Cys	Gly Lys Val Ser Lys	Ser Ser Phe Ala Lys Cys			
	560		565		570
Glu Met Arg Asp	Ala Lys Cys Gly Lys	Ile Gln Cys Gln Gly Gly			
	575		580		585
Ala Ser Arg Pro	Val Ile Gly Thr Asn	Ala Val Ser Ile Glu Thr			
	590		595		600
Asn Ile Pro Leu	Gln Gln Gly Gly Arg	Ile Leu Cys Arg Gly Thr			
	605		610		615
His Val Tyr Leu	Gly Asp Asp Met Pro	Asp Pro Gly Leu Val Leu			
	620		625		630
Ala Gly Thr Lys	Cys Ala Asp Gly Lys	Ile Cys Leu Asn Arg Gln			
	635		640		645
Cys Gln Asn Ile	Ser Val Phe Gly Val	His Glu Cys Ala Met Gln			
	650		655		660
Cys His Gly Arg	Gly Val Cys Asn Asn	Arg Lys Asn Cys His Cys			
	665		670		675
Glu Ala His Trp	Ala Pro Pro Phe Cys	Asp Lys Phe Gly Phe Gly			
	680		685		690
Gly Ser Thr Asp	Ser Gly Pro Ile Arg	Gln Ala Glu Ala Arg Gln			
	695		700		705
Glu Ala Ala Glu	Ser Asn Arg Glu Arg	Gly Gln Gly Gln Glu Pro			
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Val Gly Ser Gln	Glu His Ala Ser Thr	Ala Ser Leu Thr Leu Ile			
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<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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 ctacccagga agtttgcaga aacagtgcaa ggaagggcag ganttcctgg 150
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<400> 77
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 tacctgcacg atgggcac 18

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<400> 79
cactgggcac ctcccttc 18

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<400> 80
ctccaggctg gtctccaagt ccttcc 26

<210> 81
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<400> 81
tccctgttgg actctgcagc ttcc 24

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cttcgctggg aagagtttg 19

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<212> PRT
<213> Homo sapiens

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20 25 30
Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser
35 40 45
Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
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<400> 86
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<210> 87
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ggtagagatg tagaaggga agcaagacc 29

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<213> Homo sapiens

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 ttaaaggaaa tctttattaa tcacgtatgg ttcacagata attctttttt 2800
 taaaaaaacc caacctccta gagaagcaca actgtcaaga gtcttgtaca 2850
 cacaacttca gctttgcatc acgagtcttg tattccaaga aaatcaaagt 2900
 ggtacaattt gtttgtttac actatgatac tttctaaata aactcttttt 2950
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<210> 90
 <211> 432
 <212> PRT
 <213> Homo sapiens

<400> 90
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 Ala Ala Leu Thr Ala Leu Leu Leu Leu Leu Leu Gly His Gly Gly
 20 25 30
 Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala
 35 40 45
 Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro
 50 55 60
 His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile
 65 70 75
 Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly
 80 85 90
 His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys
 95 100 105
 Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp
 110 115 120
 Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly
 125 130 135
 Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys
 140 145 150
 Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu
 155 160 165
 Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu
 170 175 180

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Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser
				185					190					195
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile
				200					205					210
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro
				215					220					225
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val
				230					235					240
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser
				245					250					255
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp
				260					265					270
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser
				275					280					285
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly
				290					295					300
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala
				305					310					315
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn
				320					325					330
Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe
				335					340					345
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp
				350					355					360
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys
				365					370					375
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys
				380					385					390
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly
				395					400					405
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu
				410					415					420
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu			
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<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 91
atgttcttcg cgccctggtg 20

<210> 92
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 92
ccaagccaac acactctaca g 21

<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
aagtggtcgc cttgtgcaac gtgc 24

<210> 94
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
gggtcaaagg gatatatcgc cac 23

<210> 95
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96
<211> 1016
<212> DNA
<213> Homo sapiens

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gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150

atttcaccag gacccaaagg agatgatggt gaaaaaggag atccaggaga 200
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gagaactggg tgatatggga gatcagggca atattggcaa gactgggccc 300
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ttgttggaaca actggatatt agtattgctc ggctcaagac atctatgaag 450
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aaaaaaaaaa aaaaaa 1016

<210> 97
<211> 277
<212> PRT
<213> Homo sapiens

<400> 97
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Leu Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile
20 25 30
Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
35 40 45
Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
50 55 60
Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
65 70 75
Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys

80					85					90				
Thr	Gly	Pro	Ile	Gly	Lys	Lys	Gly	Asp	Lys	Gly	Glu	Lys	Gly	Leu
				95					100					105
Leu	Gly	Ile	Pro	Gly	Glu	Lys	Gly	Lys	Ala	Gly	Thr	Val	Cys	Asp
				110					115					120
Cys	Gly	Arg	Tyr	Arg	Lys	Phe	Val	Gly	Gln	Leu	Asp	Ile	Ser	Ile
				125					130					135
Ala	Arg	Leu	Lys	Thr	Ser	Met	Lys	Phe	Val	Lys	Asn	Val	Ile	Ala
				140					145					150
Gly	Ile	Arg	Glu	Thr	Glu	Glu	Lys	Phe	Tyr	Tyr	Ile	Val	Gln	Glu
				155					160					165
Glu	Lys	Asn	Tyr	Arg	Glu	Ser	Leu	Thr	His	Cys	Arg	Ile	Arg	Gly
				170					175					180
Gly	Met	Leu	Ala	Met	Pro	Lys	Asp	Glu	Ala	Ala	Asn	Thr	Leu	Ile
				185					190					195
Ala	Asp	Tyr	Val	Ala	Lys	Ser	Gly	Phe	Phe	Arg	Val	Phe	Ile	Gly
				200					205					210
Val	Asn	Asp	Leu	Glu	Arg	Glu	Gly	Gln	Tyr	Met	Ser	Thr	Asp	Asn
				215					220					225
Thr	Pro	Leu	Gln	Asn	Tyr	Ser	Asn	Trp	Asn	Glu	Gly	Glu	Pro	Ser
				230					235					240
Asp	Pro	Tyr	Gly	His	Glu	Asp	Cys	Val	Glu	Met	Leu	Ser	Ser	Gly
				245					250					255
Arg	Trp	Asn	Asp	Thr	Glu	Cys	His	Leu	Thr	Met	Tyr	Phe	Val	Cys
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Glu	Phe	Ile	Lys	Lys	Lys	Lys								
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<210> 98
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 98
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<210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccatacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

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gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200

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gcgccctggc cgcggctgcc gccgaccgg aaggtcccga ggggggctgc 450

agcctggcct ggcgctcgc ggaactggcc cagcagcgcg ccgcgcacac 500

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 catggcccaa cttgtttatt gcag 2574

<210> 102
 <211> 730
 <212> PRT
 <213> Homo sapiens

<400> 102
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 Gln Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly
 20 25 30
 Met Phe Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala
 35 40 45
 Gly Ser Met Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu
 50 55 60
 Pro Leu Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp
 65 70 75
 Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys
 80 85 90
 Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Asp Pro
 95 100 105
 Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu
 110 115 120
 Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser
 125 130 135
 Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala
 140 145 150
 Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp
 155 160 165
 Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala
 170 175 180
 Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe
 185 190 195
 Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro
 200 205 210

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Leu Ser Pro Gly	Ala Thr Val Ala Leu	Leu Leu Pro Ala Gly	Pro
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Glu Phe Leu Trp	Leu Trp Phe Gly Leu	Ala Lys Ala Gly Leu	Arg
	230	235	240
Thr Ala Phe Val	Pro Thr Ala Leu Arg	Arg Gly Pro Leu Leu	His
	245	250	255
Cys Leu Arg Ser	Cys Gly Ala Arg Ala	Leu Val Leu Ala Pro	Glu
	260	265	270
Phe Leu Glu Ser	Leu Glu Pro Asp Leu	Pro Ala Leu Arg Ala	Met
	275	280	285
Gly Leu His Leu	Trp Ala Ala Gly Pro	Gly Thr His Pro Ala	Gly
	290	295	300
Ile Ser Asp Leu	Leu Ala Glu Val Ser	Ala Glu Val Asp Gly	Pro
	305	310	315
Val Pro Gly Tyr	Leu Ser Ser Pro Gln	Ser Ile Thr Asp Thr	Cys
	320	325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr Thr	Gly Leu Pro Lys Ala	Ala
	335	340	345
Arg Ile Ser His	Leu Lys Ile Leu Gln	Cys Gln Gly Phe Tyr	Gln
	350	355	360
Leu Cys Gly Val	His Gln Glu Asp Val	Ile Tyr Leu Ala Leu	Pro
	365	370	375
Leu Tyr His Met	Ser Gly Ser Leu Leu	Gly Ile Val Gly Cys	Met
	380	385	390
Gly Ile Gly Ala	Thr Val Val Leu Lys	Ser Lys Phe Ser Ala	Gly
	395	400	405
Gln Phe Trp Glu	Asp Cys Gln Gln His	Arg Val Thr Val Phe	Gln
	410	415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu	Val Asn Gln Pro Pro	Ser
	425	430	435
Lys Ala Glu Arg	Gly His Lys Val Arg	Leu Ala Val Gly Ser	Gly
	440	445	450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe	Val Arg Arg Phe Gly	Pro
	455	460	465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu	Thr Glu Gly Asn Val	Ala
	470	475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly	Ala Val Gly Arg Ala	Ser
	485	490	495
Trp Leu Tyr Lys	His Ile Phe Pro Phe	Ser Leu Ile Arg Tyr	Asp

500	505	510
Val Thr Thr Gly Glu Pro Ile Arg Asp 515	Pro Gln Gly His Cys Met 520	
Ala Thr Ser Pro Gly Glu Pro Gly Leu 530	Leu Val Ala Pro Val Ser 535	
Gln Gln Ser Pro Phe Leu Gly Tyr Ala 545	Gly Gly Pro Glu Leu Ala 550	
Gln Gly Lys Leu Leu Lys Asp Val Phe 560	Arg Pro Gly Asp Val Phe 565	
Phe Asn Thr Gly Asp Leu Leu Val Cys 575	Asp Asp Gln Gly Phe Leu 580	
Arg Phe His Asp Arg Thr Gly Asp Thr 590	Phe Arg Trp Lys Gly Glu 595	
Asn Val Ala Thr Thr Glu Val Ala Glu 605	Val Phe Glu Ala Leu Asp 610	
Phe Leu Gln Glu Val Asn Val Tyr Gly 620	Val Thr Val Pro Gly His 625	
Glu Gly Arg Ala Gly Met Ala Ala Leu 635	Val Leu Arg Pro Pro His 640	
Ala Leu Asp Leu Met Gln Leu Tyr Thr 650	His Val Ser Glu Asn Leu 655	
Pro Pro Tyr Ala Arg Pro Arg Phe Leu 665	Arg Leu Gln Glu Ser Leu 670	
Ala Thr Thr Glu Thr Phe Lys Gln Gln 680	Lys Val Arg Met Ala Asn 685	
Glu Gly Phe Asp Pro Ser Thr Leu Ser 695	Asp Pro Leu Tyr Val Leu 700	
Asp Gln Ala Val Gly Ala Tyr Leu Pro 710	Leu Thr Thr Ala Arg Tyr 715	
Ser Ala Leu Leu Ala Gly Asn Leu Arg 725	Ile 730	

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

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<210> 104
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 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 104
 ggagaatgtg gccacaac 18

<210> 105
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 <212> DNA
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<220>
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<400> 105
 gccctggcac agtgactcca tagacg 26

<210> 106
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<400> 106
 atccacttca gcggacac 18

<210> 107
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<210> 108
 <211> 2579
 <212> DNA
 <213> Homo sapiens

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 ttgtttattc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500
 ttcttacctt catttgcttt tatgctgcag aagtaaagga atctcacgtt 2550
 gtgagggttt tttttttctc atttaaaat 2579

<210> 109
 <211> 555
 <212> PRT
 <213> Homo sapiens

<400> 109
 Met Pro Ser Trp Ile Gly Ala Val Ile Leu Pro Leu Leu Gly Leu
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 Leu Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys
 20 25 30
 Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala
 35 40 45
 Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys
 50 55 60
 Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu
 65 70 75

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	
				80					85					90	
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	
				95					100					105	
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	
				110					115					120	
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	
				125					130					135	
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	
				140					145					150	
Thr	Gly	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	
				155					160					165	
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Leu	Ile	Asn	Pro	Gln	Tyr	
				170					175					180	
His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Asp	
				185					190					195	
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Ile	Gln	
				200					205					210	
Val	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Arg	Thr	Phe	Val	Gln	Gly	Leu	
				215					220					225	
Thr	Val	Gly	Arg	Glu	Val	Ala	Asn	Arg	Val	Ser	Lys	Val	Ser	Pro	
				230					235					240	
Thr	Pro	Gly	Cys	Ile	Arg	Ala	Leu	Met	Lys	Met	Leu	Tyr	Cys	Pro	
				245					250					255	
Tyr	Cys	Arg	Gly	Leu	Pro	Thr	Val	Arg	Pro	Cys	Asn	Asn	Tyr	Cys	
				260					265					270	
Leu	Asn	Val	Met	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	
				275					280					285	
Thr	Glu	Trp	Asn	Leu	Phe	Ile	Asp	Ala	Met	Leu	Leu	Val	Ala	Glu	
				290					295					300	
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile	
				305					310					315	
Asp	Val	Lys	Ile	Ser	Glu	Ala	Ile	Met	Asn	Met	Gln	Glu	Asn	Ser	
				320					325					330	
Met	Gln	Val	Ser	Ala	Lys	Val	Phe	Gln	Gly	Cys	Gly	Gln	Pro	Lys	
				335					340					345	
Pro	Ala	Pro	Ala	Leu	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Glu	Asn	Phe	
				350					355					360	
Asn	Thr	Arg	Phe	Arg	Pro	Tyr	Asn	Pro	Glu	Glu	Arg	Pro	Thr	Thr	

365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu	Val Thr Asp Ile Lys Glu	
380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp	Ser Ala Leu Pro Tyr Thr	
395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala	Gly Thr Ser Asn Glu Glu	
410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala	Arg Tyr Leu Pro Glu Ile	
425	430	435
Met Asn Asp Gly Leu Thr Asn Gln Ile	Asn Asn Pro Glu Val Asp	
440	445	450
Val Asp Ile Thr Arg Pro Asp Thr Phe	Ile Arg Gln Gln Ile Met	
455	460	465
Ala Leu Arg Val Met Thr Asn Lys Leu	Lys Asn Ala Tyr Asn Gly	
470	475	480
Asn Asp Val Asn Phe Gln Asp Thr Ser	Asp Glu Ser Ser Gly Ser	
485	490	495
Gly Ser Gly Ser Gly Cys Met Asp Asp	Val Cys Pro Thr Glu Phe	
500	505	510
Glu Phe Val Thr Thr Glu Ala Pro Ala	Val Asp Pro Asp Arg Arg	
515	520	525
Glu Val Asp Ser Ser Ala Ala Gln Arg	Gly His Ser Leu Leu Ser	
530	535	540
Trp Ser Leu Thr Cys Ile Val Leu Ala	Leu Gln Arg Leu Cys Arg	
545	550	555

<210> 110
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 110
 aagcgtgaca gcgggcacgt c 21

<210> 111
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 111

tgcacagtct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgacctg 40

<210> 113

<211> 4649

<212> DNA

<213> Homo sapiens

<400> 113

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aataagtttag ctgagaaaac gcacgcagtt tgcagcgcct gcgccgggtg 100

cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150

tagggacccg gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200

tgctgcccgg agtttctgcg gaggtggagg gagatcagga aacggcttct 250

tcctcacttc gccgcctggt gagtgtcggg gagattggca aacgcctagg 300

aaaggactgg ggaaaaatagc cctgggaaaag tggagaaggt gatcaggagg 350

ccggtccact acggcagttt atctgtctga tcagagccag acgcgacgcg 400

tccacttcgc agttctttcc aggtgtgggg accgcaggac agacggcccga 450

tcccgcgcc ctccgtacca gcaactcccag gagagtcagc ctgctcccc 500

aacgtcgagg gcgctctggc cacgaaaagt tcctgtccac tgtgattctc 550

aattccttgc ttggtttttt tctccagaga acttttgggt ggagatatta 600

acttttttct tttttttttt ccttgggtgga agctgctcta gggagggggg 650

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cttccggagt cccatccatt aagccatcac ttctggaaga ttaaagttgt 750

cggacatggt gacagctgag aggagaggag gatttcttgc cagggtggaga 800

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 taactggcct ctgagaggta gcaaaggaac atattgggaa ggagggatcc 1950
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<210> 114
 <211> 515
 <212> PRT
 <213> Homo sapiens

<400> 114
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 1 5 10 15
 Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala Met Gly Ala Leu
 20 25 30
 Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser
 35 40 45
 Trp Gly Gln Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu Leu Ala
 50 55 60
 Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln
 65 70 75
 Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp
 80 85 90
 Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys
 95 100 105
 Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro

110	115	120
Ile Cys Thr Pro Ser Arg Ser Gln Phe	Ile Thr Gly Lys Tyr Gln	
125	130	135
Ile His Thr Gly Leu Gln His Ser Ile	Ile Arg Pro Thr Gln Pro	
140	145	150
Asn Cys Leu Pro Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys	
155	160	165
Glu Val Gly Tyr Ser Thr His Met Val	Gly Lys Trp His Leu Gly	
170	175	180
Phe Asn Arg Lys Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr	
185	190	195
Phe Phe Gly Ser Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr	
200	205	210
Lys Cys Asp Ser Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn	
215	220	225
Asp Asn Ala Ala Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln	
230	235	240
Met Tyr Thr Gln Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro	
245	250	255
Thr Lys Pro Ile Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser	
260	265	270
Pro Leu Gln Ala Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile	
275	280	285
Ile Asn Ile Asn Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu	
290	295	300
Asp Glu Ala Ile Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly	
305	310	315
Phe Tyr Asn Asn Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly	
320	325	330
Gln Pro Thr Ala Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys	
335	340	345
Gly Thr Tyr Trp Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His	
350	355	360
Ser Pro Leu Leu Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val	
365	370	375
His Ile Thr Asp Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly	
380	385	390
Gln Ile Asp Glu Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu	
395	400	405

Thr Ile Ser Glu Gly Leu Arg Ser Pro Arg Val Asp Ile Leu His
 410 415 420
 Asn Ile Asp Pro Tyr Thr Pro Arg Gln Lys Met Ala Pro Gly Gln
 425 430 435
 Gln Ala Met Gly Ser Gly Thr Leu Gln Ser Ser Gln Pro Ser Glu
 440 445 450
 Cys Ser Thr Gly Asn Cys Leu Gln Glu Ile Leu Ala Thr Ala Thr
 455 460 465
 Gly Ser Pro Leu Ser Leu Ser Ala Thr Trp Asp Arg Thr Gly Gly
 470 475 480
 Thr Met Asn Gly Ser Pro Cys Gln Leu Ala Lys Val Tyr Gly Phe
 485 490 495
 Ser Thr Ser Gln Pro Thr His Met Arg Gly Trp Thr Tyr Leu Thr
 500 505 510
 Gly Ile Gln Glu Ser
 515

<210> 115
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 115
 cccaacccaa ctgtttacct ctgg 24

<210> 116
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 116
 ctctctgagt gtacatctgt gtgg 24

<210> 117
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<220>
 <221> unsure
 <222> 33
 <223> unknown base

<400> 117
gccaccctac ctcagaaact gaaggagggt ggntattcaa cgcataatggt 50

cgg 53

<210> 118
<211> 2260
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086
<223> unknown base

<400> 118
cggacgcgtg ggtgcgagtg gagcggagga cccgagcggc tgaggagaga 50
ggaggcggcg gcttagctgc tacgggggtcc ggccggcgcc ctcccagggg 100
gggctcagga ggaggaagga ggaccgcgtg gagaatgcct ctgccctgga 150
gccttgcgt cccgctgctg ctctcctggg tggcagggtg tttcggaac 200
gcggccagt caaggcatca cgggttgta gcatcggcac gtcagcctgg 250
ggtctgtcac tatggaacta aactggcctg ctgctacggc tggagaagaa 300
acagcaaggg agtctgtgaa gctacatgcg aacctggatg taagtttggt 350
gagtgcgtgg gaccaaacia atgcagatgc tttccaggat acaccgggaa 400
aacctgcagt caagatgtga atgagtgtgg aatgaaaccc cggccatgcc 450
aacacagatg tgtgaataca cacggaagct acaagtgcct ttgcctcagt 500
ggccacatgc tcatgccaga tgctacgtgt gtgaactcta ggacatgtgc 550
catgataaac tgtcagtaca gctgtgaaga cacagaagaa gggccacagt 600
gcctgtgtcc atcctcagga ctccgcctgg ccccaaattg aagagactgt 650
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aagatgtgtg aacacatttg gaagctacta ctgcaaattg cacattgggt 750
tcgaactgca atatatcagt ggacgatatg actgtataga tataaatgaa 800
tgtactatgg atagccatac gtgcagccac catgccaatt gcttcaatac 850
ccaaggggtc ttcaagtgtg aatgcaagca gggatataaa ggcaatggac 900
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cctggtacca tcaaagacag aatcaagaag ttgcttgctc acaaaaacag 1000
catgaaaaag aaggcaaaaa ttaaaaatgt taccacagaa cccaccagga 1050

ctcctacccc taaggtgaac ttgcagccct tcaactatga agagatagtt 1100
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 catagaggag cgaagcctgc gaggagatgt gtttttccct aaggtgaatg 1250
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 aagtggctta gctgggtctt tcatagccaa acttgtatat ttaattcttt 2250
 gtaataataa 2260

<210> 119
 <211> 338
 <212> PRT
 <213> Homo sapiens

<400> 119
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Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	
				35					40					45	
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	
				50					55					60	
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
				65					70					75	
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	
				80					85					90	
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
				95					100					105	
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	
				110					115					120	
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	
				125					130					135	
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	
				140					145					150	
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	
				155					160					165	
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	
				170					175					180	
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
				185					190					195	
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	
				200					205					210	
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	
				215					220					225	
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	
				230					235					240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	
				245					250					255	
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	
				260					265					270	
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	
				275					280					285	
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
				290					295					300	
Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	

	305		310		315
Phe Asn Tyr Glu	Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly				
	320		325		330
Gly Lys Lys Gly	Asn Glu Glu Lys				
	335				

<210> 120
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 120
 cctcagtggc cacatgctca tg 22

<210> 121
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 121
 ggctgcacgt atggctatcc atag 24

<210> 122
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 122
 gataaactgt cagtacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 123
 <211> 1199
 <212> DNA
 <213> Homo sapiens

<400> 123
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 ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatgggtg 150
 tgtgggtgac tggagcctcg agtgaattg gtgaggagct ggcttaccag 200
 ttgtctaaac taggagtttc tcttgtgctg tcagccagaa gagtgcata 250
 gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300

aagatatact tgttttggccc cttgacctga ccgacactgg ttcccatgaa 350
 gcggctacca aagctgttct ccaggagttt ggtagaatcg acattctggt 400
 caacaatggt ggaatgtccc agcgttctct gtgcatggat accagcttgg 450
 atgtctacag aaagctaata gagcttaact acttagggac ggtgtccttg 500
 acaaaatgtg ttctgcctca catgatcgag aggaagcaag gaaagattgt 550
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 gtgcggctga tgttaatcag catggccaat gatttgaaag aagtttggat 850
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 ttttaagagt gtgtggatgc agactcttct tattttaaaa tctttaagac 1000
 aaaacatgac tgaaaagagc acctgtactt ttcaagccac tggagggaga 1050
 aatggaaaac atgaaaacag caatcttctt atgcttctga ataataaaag 1100
 actaatttgt gattttactt tttaatagat atgactttgc ttccaacatg 1150
 gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124
 <211> 289
 <212> PRT
 <213> Homo sapiens

<400> 124
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 20 25 30
 Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu
 35 40 45
 Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu
 50 55 60
 Asp Leu Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val
 65 70 75
 Leu Gln Glu Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly

80										85					90				
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr					
				95					100					105					
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr					
				110					115					120					
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile					
				125					130					135					
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser					
				140					145					150					
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn					
				155					160					165					
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser					
				170					175					180					
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser					
				185					190					195					
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln					
				200					205					210					
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile					
				215					220					225					
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro					
				230					235					240					
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala					
				245					250					255					
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe					
				260					265					270					
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys					
				275					280					285					

Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126
ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127
cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128
ctgtagacat ccaagctggg atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129
aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130
acctgacgct actatggggc gagtggcagg gacgacgccc agaatg 46

<210> 131

<211> 2365

<212> DNA

<213> Homo sapiens

<400> 131

gcgacgtggg caccgccatc agctgttcgc gcgtcttctc ctccaggtgg 50
ggcagggggtt tcgggctggt ggagcatgtg ctgggacagg acagcatcct 100
caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150
tgtaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200
tccctggtgt ctctcgctgg ttctgtctac ctggcctgga tcctgttctt 250
cgtgctctat gatttctgca ttgtttgtat caccacctat gctatcaacg 300
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 cctcctttac tctttcagat acaatcacgc cagccacgtt gttttgaaaa 2300
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 tgttacaaaa taaaa 2365

<210> 132
 <211> 571
 <212> PRT
 <213> Homo sapiens

<400> 132
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 20 25 30
 Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe
 35 40 45
 Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn
 50 55 60
 Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln
 65 70 75

Gly	Ala	His	Ile	Cys	Ser	Gly	Ser	Leu	Val	Ala	Asp	Thr	Trp	Val	
				80					85					90	
Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Lys	Ala	Ala	Ala	Thr	Glu	Leu	
				95					100					105	
Asn	Ser	Trp	Ser	Val	Val	Leu	Gly	Ser	Leu	Gln	Arg	Glu	Gly	Leu	
				110					115					120	
Ser	Pro	Gly	Ala	Glu	Glu	Val	Gly	Val	Ala	Ala	Leu	Gln	Leu	Pro	
				125					130					135	
Arg	Ala	Tyr	Asn	His	Tyr	Ser	Gln	Gly	Ser	Asp	Leu	Ala	Leu	Leu	
				140					145					150	
Gln	Leu	Ala	His	Pro	Thr	Thr	His	Thr	Pro	Leu	Cys	Leu	Pro	Gln	
				155					160					165	
Pro	Ala	His	Arg	Phe	Pro	Phe	Gly	Ala	Ser	Cys	Trp	Ala	Thr	Gly	
				170					175					180	
Trp	Asp	Gln	Asp	Thr	Ser	Asp	Ala	Pro	Gly	Thr	Leu	Arg	Asn	Leu	
				185					190					195	
Arg	Leu	Arg	Leu	Ile	Ser	Arg	Pro	Thr	Cys	Asn	Cys	Ile	Tyr	Asn	
				200					205					210	
Gln	Leu	His	Gln	Arg	His	Leu	Ser	Asn	Pro	Ala	Arg	Pro	Gly	Met	
				215					220					225	
Leu	Cys	Gly	Gly	Pro	Gln	Pro	Gly	Val	Gln	Gly	Pro	Cys	Gln	Gly	
				230					235					240	
Asp	Ser	Gly	Gly	Pro	Val	Leu	Cys	Leu	Glu	Pro	Asp	Gly	His	Trp	
				245					250					255	
Val	Gln	Ala	Gly	Ile	Ile	Ser	Phe	Ala	Ser	Ser	Cys	Ala	Gln	Glu	
				260					265					270	
Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn	Thr	Ala	Ala	His	Ser	Ser	Trp	
				275					280					285	
Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala	Phe	Leu	Ala	Gln	Ser	Pro	
				290					295					300	
Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser	Cys	Val	Ala	Cys	Gly	
				305					310					315	
Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	
				320					325					330	
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	
				335					340					345	
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	
				350					355					360	
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	

	365		370		375
Thr Arg Pro Glu	Glu Trp Gly Leu Lys	Gln Leu Ile Leu His	Gly		
	380	385	390		
Ala Tyr Thr His	Pro Glu Gly Gly Tyr	Asp Met Ala Leu Leu	Leu		
	395	400	405		
Leu Ala Gln Pro	Val Thr Leu Gly Ala	Ser Leu Arg Pro Leu	Cys		
	410	415	420		
Leu Pro Tyr Pro	Asp His His Leu Pro	Asp Gly Glu Arg Gly	Trp		
	425	430	435		
Val Leu Gly Arg	Ala Arg Pro Gly Ala	Gly Ile Ser Ser Leu	Gln		
	440	445	450		
Thr Val Pro Val	Thr Leu Leu Gly Pro	Arg Ala Cys Ser Arg	Leu		
	455	460	465		
His Ala Ala Pro	Gly Gly Asp Gly Ser	Pro Ile Leu Pro Gly	Met		
	470	475	480		
Val Cys Thr Ser	Ala Val Gly Glu Leu	Pro Ser Cys Glu Gly	Leu		
	485	490	495		
Ser Gly Ala Pro	Leu Val His Glu Val	Arg Gly Thr Trp Phe	Leu		
	500	505	510		
Ala Gly Leu His	Ser Phe Gly Asp Ala	Cys Gln Gly Pro Ala	Arg		
	515	520	525		
Pro Ala Val Phe	Thr Ala Leu Pro Ala	Tyr Glu Asp Trp Val	Ser		
	530	535	540		
Ser Leu Asp Trp	Gln Val Tyr Phe Ala	Glu Glu Pro Glu Pro	Glu		
	545	550	555		
Ala Glu Pro Gly	Ser Cys Leu Ala Asn	Ile Ser Gln Pro Thr	Ser		
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Cys

<210> 133
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 133
 cctgtgctgt gcctcgagcc tgac 24

<210> 134
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gtagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggccgccc ccggcccca ttggggccgg gcctcgctgc ggccggcgact 50

gagccaggct ggcccgctc cctgagtcac agagtcggcg cggcgccgca 100

ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150

gatgctgctg cgccggggca gccctggcat ggggtgtgcat gtgggtgcag 200

ccctgggagc actgtggttc tgcctcacag gagccctgga ggtccaggctc 250

cctgaagacc cagtgtgtgc actgtgtggc accgatgcca ccctgtgctg 300

ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350

ggcagctgac agatacaaaa cagctggtgc acagctttgc tgagggccag 400

gaccagggca gcgcctatgc caaccgcacg gccctcttcc cggacctgct 450

ggcacagggc aacgcacccc tgaggctgca gcgcgtgctg gtggcggacg 500

agggcagctt cacctgcttc gtgagcatcc gggatttcgg cagcgtgctc 550

gtcagcctgc aggtggccgc tccctactcg aagcccagca tgaccctgga 600

gccaacaag gacctgcggc caggggacac ggtgaccatc acgtgctcca 650

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cttgtttgat gtgcacagcg tctgcggggt ggtgctgggt gcgaatggca 800

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 agacagggca gggccaggaa tgctttgggg acaccgaggg gactgcccc 1750
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 atgccttccg gatgtcatct ctccctgccc caggaatgga agatgtgagg 1900
 acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950
 attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

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09978187 101501

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Val Gln Val Pro	Glu Asp Pro Val Val	Ala Leu Val Gly Thr	Asp
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Ala Thr Leu Cys	Cys Ser Phe Ser Pro	Glu Pro Gly Phe Ser	Leu
50		55	60
Ala Gln Leu Asn	Leu Ile Trp Gln Leu	Thr Asp Thr Lys Gln	Leu
65		70	75
Val His Ser Phe	Ala Glu Gly Gln Asp	Gln Gly Ser Ala Tyr	Ala
80		85	90
Asn Arg Thr Ala	Leu Phe Pro Asp Leu	Leu Ala Gln Gly Asn	Ala
95		100	105
Ser Leu Arg Leu	Gln Arg Val Arg Val	Ala Asp Glu Gly Ser	Phe
110		115	120
Thr Cys Phe Val	Ser Ile Arg Asp Phe	Gly Ser Ala Ala Val	Ser
125		130	135
Leu Gln Val Ala	Ala Pro Tyr Ser Lys	Pro Ser Met Thr Leu	Glu
140		145	150
Pro Asn Lys Asp	Leu Arg Pro Gly Asp	Thr Val Thr Ile Thr	Cys
155		160	165
Ser Ser Tyr Gln	Gly Tyr Pro Glu Ala	Glu Val Phe Trp Gln	Asp
170		175	180
Gly Gln Gly Val	Pro Leu Thr Gly Asn	Val Thr Thr Ser Gln	Met
185		190	195
Ala Asn Glu Gln	Gly Leu Phe Asp Val	His Ser Val Leu Arg	Val
200		205	210
Val Leu Gly Ala	Asn Gly Thr Tyr Ser	Cys Leu Val Arg Asn	Pro
215		220	225
Val Leu Gln Gln	Asp Ala His Xaa Ser	Val Thr Ile Thr Gly	Gln
230		235	240
Pro Met Thr Phe	Pro Pro Glu Ala Leu	Trp Val Thr Val Gly	Leu
245		250	255
Ser Val Cys Leu	Ile Ala Leu Leu Val	Ala Leu Ala Phe Val	Cys
260		265	270
Trp Arg Lys Ile	Lys Gln Ser Cys Glu	Glu Glu Asn Ala Gly	Ala
275		280	285
Glu Asp Gln Asp	Gly Glu Gly Glu Gly	Ser Lys Thr Ala Leu	Gln
290		295	300

Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
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Ala

<210> 138
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 138
 ctggcacagc tcaacctcat ctgg 24

<210> 139
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 139
 gctgtctgtc tgtctcattg 20

<210> 140
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 140
 ggacacagta tactgaccac 20

<210> 141
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 141
 tgcgaaccag gcagctgtaa gtgc 24

<210> 142
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 142
 tggaagaaga gggtggtgat gtgg 24

<210> 143
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 143
 cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144
 <211> 2336
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 1620, 1673
 <223> unknown base

<400> 144
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 gaaggggggag tcttgaactt gtctgaagcc cttgtccgta agccttgaac 100
 tacgttctta aatctatgaa gtcgaggac ctttcgctgc ttttgtaggg 150
 acttctttcc ttgcttcagc aacatgaggc ttttcttgtg gaacgcggtc 200
 ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250
 agtgaaaatt gaagttctcc agaagccatt catctgccat cgcaagacca 300
 aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350
 ggctccttat ttcactccac tcacaaacat aacaatgggc agcccatttg 400
 gtttaccctg ggcacccctg aggtctctcaa aggttgggac cagggcttga 450
 aaggaatgtg ttaggagag aagagaaaagc tcatcattcc tctgctctg 500
 ggctatggaa aagaaggaaa aggtaaaatt cccccagaaa gtacactgat 550
 atttaatat gatctcctgg agattcgaaa tggaccaaga tcccatgaat 600
 cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650
 gttaaagcat atttaaagaa ggagtttgaa aaacatgggtg cggtggtgaa 700
 tgaaagtcac catgatgctt tgggtggagga tatttttgat aaagaagatg 750
 aagacaaaga tgggtttata tctgccagag aatttacata taaacacgat 800
 gagttataga gatacatcta cctttttaat atagcactca tctttcaaga 850

gagggcagtc atcttttaaag aacattttat ttttatacaa tggtctttct 900
tgctttgttt tttattttta tatatttttt ctgactccta tttaaagaac 950
cccttagggt tctaagtacc catttctttc tgataagtta ttgggaagaa 1000
aaagctaatt ggtctttgaa tagaagactt ctggacaatt tttcactttc 1050
acagatatga agctttgttt tacttttctca cttataaatt taaaatgttg 1100
caactgggaa tataccacga catgagacca gggtatagca caaattagca 1150
ccctatattt ctgcttccct ctattttctc caagttagag gtcaacattt 1200
gaaaagcctt ttgcaatagc ccaaggcttg ctattttcat gttataatga 1250
aatagtttat gtgtaactgg ctctgagtct ctgcttgagg accagaggaa 1300
aatggttggt ggacctgact tgttaatggc tactgcttta ctaaggagat 1350
gtgcaatgct gaagttagaa acaaggttaa tagccaggca tgggtggctca 1400
tgctgtaat ccagcactt tgggaggctg aggcgggcgg atcacctgag 1450
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accaggaag gctgaggcgg cagaatcact tgaacccgag gccgagggtg 1600
cggtaagccg agatcacctn cagcctggac actctgtctc gaaaaaagaa 1650
aagaacacgg ttaataccat atnaatatgt atgcattgag acatgctacc 1700
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gataaatagg acaaatcatt tatgtgtgag tttctttgta ataaaatgta 1800
tcaatatggt atagatgagg tagaaagtta tatttatatt caatatttac 1850
ttottaaggc tagcgggaata tccttctggt ttctttaatg ggtagtctat 1900
agtatattat actacaataa cattgtatca taagataaag tagtaaacca 1950
gtctacattt tccattttct gtctcatcaa aaactgaagt tagctgggtg 2000
tgggtggctca tgctgtaat ccagcactt tgggggcca gagggtgga 2050
tcacttgaga tcaggagtto aagaccagcc tggccaacat ggtgaaacct 2100
tgtctctact aaaaatacaa aaattagcca ggcgtggtgg tgcacacctg 2150
tagtcccagc tactcgggag gctgagacag gagatttgct tgaacccggg 2200
aggcggagggt tgcagtgagc caagattgtg ccactgcact ccagcctggg 2250
tgacagagca agactccatc tcaaaaaaaa aaaaagaag cagacctaca 2300

gcagctacta ttgaataaat acctatcctg gatttt 2336

<210> 145
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 145
 Met Arg Leu Phe Leu Trp Asn Ala Val Leu Thr Leu Phe Val Thr
 1 5 10 15
 Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu
 20 25 30
 Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly
 35 40 45
 Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly
 50 55 60
 Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile
 65 70 75
 Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln
 80 85 90
 Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile
 95 100 105
 Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro
 110 115 120
 Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg
 125 130 135
 Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn
 140 145 150
 Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys
 155 160 165
 Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His
 170 175 180
 Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys
 185 190 195
 Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu
 200 205 210

Leu

<210> 146
 <211> 26
 <212> DNA
 <213> Artificial Sequence

09978137-101501

<220>
<223> Synthetic oligonucleotide probe

<400> 146
ctttccttgc ttcagcaaca tgaggc 26

<210> 147
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 147
gccagagca ggaggaatga tgagc 25

<210> 148
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 148
gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149
<211> 2196
<212> DNA
<213> Homo sapiens

<400> 149
aataaagctt ccttaatggt gtatatgtct ttgaagtaca tccgtgcatt 50
tttttttagc atccaacat tctcccttg tagttctcgc cccctcaa 100
caccctctcc cgtagccac ccgactaaca tctcagtc tgaatgca 150
cagagatgcc tggctacctc gccctgcctt cagcctcagc gggctcagtc 200
tctttttctc tttggtgcc caggacgga gcatggaggc cacagtacct 250
gccaccctca acgtctcaa tggctctgac gcccgctgc cctgcacctt 300
caactcctgc tacacagtga accacaaaca gttctccctg aactggactt 350
accaggagtgc caacaactgc tctgaggaga tgttctcca gttccgcatg 400
aagatcatta acctgaagct ggagcgggtt caagaccgcg tggagttctc 450
agggaaaccc agcaagtacg atgtgtcggg gatgctgaga aacgtgcagc 500
cggaggatga ggggatttac aactgctaca tcatgaaccc cctgaccgc 550
caccgtggcc atggcaagat ccatctgcag gtcctcatgg aagagcccc 600

tgagcgggac tccacggtgg ccgtgattgt gggcgcctcc gtcgggggct 650
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 aaaaaagagc agaagctgag cacagatgac ctgaagaccg aggaggaggg 750
 caagacggac ggtgaaggca acccgatga tggcgccaag tagtgggtgg 800
 ccggccctgc agcctcccggt gtcccgtctc ctcccctctc cgccctgtac 850
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 caccaagagt gaccactct cttccatccg agaaacctgc catgctctgg 1000
 gacgtgtggg ccctggggag aggagagaaa gggctccac ctgccagtcc 1050
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 ggtgggcagg ggtagaggag gggccgctgt cacctgccca gtgcttgcc 1150
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 aggttgctgc aggtctgccc ttctccatgg ggtaaccacc ctgcctggg 1650
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 gctttctttg gggttcagt gagaactctc ccagttgccc ttgggtgggt 1750
 ttccacctgg cttttggcta cagagaggga agggaaagcc tgaggccggc 1800
 ataaggggag gccttggaac ctgagctgcc aatgccagcc ctgtcccatc 1850
 tgcggccacg ctactcgctc ctctcccaac aactcccttc gtgggggacaa 1900
 aagtgacaat tgtaggccag gcacagtggc tcacgcctgt aatcccagca 1950
 ctttgggagg ccaaggcggg tggattacct ccactgttt agtagaaatg 2000
 ggcaaaaccc catctctact aaaaatacaa gaattagctg ggcgtgggtg 2050

cggtgtgcctg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100
 tgagccccggg aagcagaggt tgcagtgaac tgagatagtg atagtgccac 2150
 tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 150
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 Gly Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met
 20 25 30
 Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp
 35 40 45
 Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His
 50 55 60
 Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys
 65 70 75
 Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu
 80 85 90
 Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro
 95 100 105
 Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu
 110 115 120
 Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg
 125 130 135
 His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu
 140 145 150
 Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser
 155 160 165
 Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val
 170 175 180
 Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp
 185 190 195
 Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro
 200 205 210
 Asp Asp Gly Ala Lys
 215

<210> 151

<211> 524
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 103, 233
 <223> unknown base

<400> 151
 gttgtatatg tcttgaagta catccgtgca ttttttttag catccaacca 50
 tcttcccttg tagttctcgc cccctcaaat caccttctcc cttagccac 100
 ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150
 gccctgcctt cagcctcacg gggctcagtc tctttttctc ttgggtgcca 200
 ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250
 aatggctctg acgcccgcct gccctgccct tcaactcctg ctacacagtg 300
 aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350
 ctctgaggag atgttctctc agttccgcat gaagatcatt aacctgaagc 400
 tggagcgggt tcaagaccgc gtggagttct cagggaacct cagcaagtac 450
 gatgtgtcgg tgatgtctgag aaacgtgcag ccggaggatg aggggattta 500
 caactgctac atcatgaacc cccc 524

<210> 152
 <211> 368
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 56, 123
 <223> unknown base

<400> 152
 tcacggggct catctctttt tctcttttgt gccaccagg acggagcatg 50
 gaggtncaca tacctgccac cctcaacgtc ctcaatggct ttgacgccg 100
 cctgccctgc accttcaact ccngctacac agtgaaccac aaacagttct 150
 cctgaactg gatttaccag gagtgaaca actggctctg aggagatgtt 200
 cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250
 ttcaagaacc gcgtggaagt ttctcagga accccagcaa gtacgatgtg 300
 tcggtgatgc tgagaaacgt gcagccggag gatgagggga tttacaactg 350
 ctacatcatg aaccccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggtccaca gtac 24

<210> 154
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
gcacgtttct cagcatcacc gac 23

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155
cgccctgccct gcaccttcaa ctccctgctac acagtgaacc acaaacagtt 50

<210> 156
<211> 2680
<212> DNA
<213> Homo sapiens

<400> 156
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cgcggaacca gcgtccccgg ccggacgtca cccccagtg gtgctgggtcc 150
ctgggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagtg 200
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gtggatgtac gtgtccctgg ctttggaag accttctcac tggagttoct 400
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tatgactggc gccgagcccc aaatgaaaac gggccctact tcctggccct 550
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 ccaaggatga gagcaggggt tggagccatg gccttctggg aacctatgga 2100
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 actagtacca agtgggtcag cacagggctg aggatggggc tcctatccac 2250
 cctggccagc acccagctta gtgctgggac tagcccagaa acttgaatgg 2300
 gaccctgaga gagccagggg tcccctgagg cccccctagg ggctttctgt 2350
 ctgccccagg gtgctccatg gatctccctg tggcagcagg catggagagt 2400
 cagggctgcc ttcattggcag taggctctaa gtgggtgact ggccacaggc 2450
 cgagaaaagg gtacagcctc taggtggggg tcccaaagac gccttcaggc 2500
 tggactgagc tgctctccca cagggtttct gtgcagctgg attttctctg 2550
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 atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157
 <211> 412
 <212> PRT
 <213> Artificial

<400> 157
 Met Gly Leu His Leu Arg Pro Tyr Arg Val Gly Leu Leu Pro Asp
 1 5 10 15
 Gly Leu Leu Phe Leu Leu Leu Leu Met Leu Leu Ala Asp Pro
 20 25 30
 Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly
 35 40 45
 Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val
 50 55 60
 Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile
 65 70 75
 Trp Leu Asn Leu Glu Leu Leu Leu Pro Val Ile Ile Asp Cys Trp
 80 85 90
 Ile Asp Asn Ile Arg Leu Val Tyr Asn Lys Thr Ser Arg Ala Thr
 95 100 105
 Gln Phe Pro Asp Gly Val Asp Val Arg Val Pro Gly Phe Gly Lys

	110		115		120
Thr Phe Ser Leu	Glu Phe Leu Asp Pro	Ser Lys Ser Ser Val	Gly		
	125		130		135
Ser Tyr Phe His	Thr Met Val Glu Ser	Leu Val Gly Trp Gly	Tyr		
	140		145		150
Thr Arg Gly Glu	Asp Val Arg Gly Ala	Pro Tyr Asp Trp Arg	Arg		
	155		160		165
Ala Pro Asn Glu	Asn Gly Pro Tyr Phe	Leu Ala Leu Arg Glu	Met		
	170		175		180
Ile Glu Glu Met	Tyr Gln Leu Tyr Gly	Gly Pro Val Val Leu	Val		
	185		190		195
Ala His Ser Met	Gly Asn Met Tyr Thr	Leu Tyr Phe Leu Gln	Arg		
	200		205		210
Gln Pro Gln Ala	Trp Lys Asp Lys Tyr	Ile Arg Ala Phe Val	Ser		
	215		220		225
Leu Gly Ala Pro	Trp Gly Gly Val Ala	Lys Thr Leu Arg Val	Leu		
	230		235		240
Ala Ser Gly Asp	Asn Asn Arg Ile Pro	Val Ile Gly Pro Leu	Lys		
	245		250		255
Ile Arg Glu Gln	Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu	Leu		
	260		265		270
Pro Tyr Asn Tyr	Thr Trp Ser Pro Glu	Lys Val Phe Val Gln	Thr		
	275		280		285
Pro Thr Ile Asn	Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe	Gln		
	290		295		300
Asp Ile Gly Phe	Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr	Glu		
	305		310		315
Gly Leu Val Glu	Ala Thr Met Pro Pro	Gly Val Gln Leu His	Cys		
	320		325		330
Leu Tyr Gly Thr	Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr	Glu		
	335		340		345
Ser Phe Pro Asp	Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly	Asp		
	350		355		360
Gly Thr Val Asn	Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp	Gln		
	365		370		375
Ser Arg Gln Glu	His Gln Val Leu Leu	Gln Glu Leu Pro Gly	Ser		
	380		385		390
Glu His Ile Glu	Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr	Leu		
	395		400		405

Lys Arg Val Leu Leu Gly Pro
410

<210> 158
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 158
ctggggctac acacggggtg agg 23

<210> 159
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 159
ggtgccgctg cagaaagtag agcg 24

<210> 160
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 160
gccccaaatg aaaacgggcc ctacttcctg gccctccgcg agatg 45

<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
cggacgcgtg ggcggacgcg tggggcggcg gcagcggcgg cgacggcgac 50
atggagagcg gggcctacgg cgcggccaag gcgggcggct ccttcgacct 100
gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150
tcttcgcctt gatcgtgttc tcttgcattc atggtgaggg ctacagcaat 200
gcccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250
ctgccgctat ggcagtgcca tcgggggtgct ggccttcctg gcctcggcct 300
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cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400

cctgtggttt gttggtttct gcttcctcac caaccagtgg gcagtcacca 450
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 gcgttctctg ccaaagactc gtgggggcca tcacacctgc cctgtgcagc 1150
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 gtgccccatg gctcccagac tctgtctgtg ccgagtgtat tataaaatcg 1450
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<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

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Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala
				20					25					30

Val Cys Leu Val Phe Ala Leu Ile Val Phe Ser Cys Ile Tyr Gly
 35 40 45
 Glu Gly Tyr Ser Asn Ala His Glu Ser Lys Gln Met Tyr Cys Val
 50 55 60
 Phe Asn Arg Asn Glu Asp Ala Cys Arg Tyr Gly Ser Ala Ile Gly
 65 70 75
 Val Leu Ala Phe Leu Ala Ser Ala Phe Phe Leu Val Val Asp Ala
 80 85 90
 Tyr Phe Pro Gln Ile Ser Asn Ala Thr Asp Arg Lys Tyr Leu Val
 95 100 105
 Ile Gly Asp Leu Leu Phe Ser Ala Leu Trp Thr Phe Leu Trp Phe
 110 115 120
 Val Gly Phe Cys Phe Leu Thr Asn Gln Trp Ala Val Thr Asn Pro
 125 130 135
 Lys Asp Val Leu Val Gly Ala Asp Ser Val Arg Ala Ala Ile Thr
 140 145 150
 Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu
 155 160 165
 Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn
 170 175 180
 Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr
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 Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln
 200 205 210
 Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr
 215 220

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 163
 tggctcttcgc cttgatcgtg ttct 24

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<400> 164
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<210> 165
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 165
ctgaaggtaga tggctgccct cac 23

<210> 166
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 166
ccaggaggct catgggaaag tcc 23

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
ccacgagtct aagcagatgt actgcgtgtt caaccgcaac gaggatgcct 50

<210> 168
<211> 3143
<212> DNA
<213> Homo sapiens

<400> 168
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ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150
atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200
cctggtgccc ctgtttgtgc tgctggccct gctcgtgctg gcttcggcgg 250
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agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450
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<210> 169
 <211> 802
 <212> PRT
 <213> Homo sapiens
 <400> 169

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Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	35	40	45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	50	55	60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	65	70	75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	80	85	90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	95	100	105	
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	110	115	120	
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	125	130	135	
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	140	145	150	
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	155	160	165	
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	170	175	180	
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile	185	190	195	
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu	200	205	210	
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	215	220	225	
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	230	235	240	
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	245	250	255	
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	260	265	270	
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	275	280	285	
Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala				

				290					295					300	
Val	Val	Trp	Lys	Lys	Gly	Leu	His	Ser	Tyr	Tyr	Asp	Pro	Phe	Val	
				305					310					315	
Leu	Ser	Val	Gln	Pro	Val	Val	Phe	Gln	Ala	Cys	Glu	Val	Asn	Leu	
				320					325					330	
Thr	Leu	Asp	Asn	Arg	Leu	Asp	Ser	Gln	Gly	Val	Leu	Ser	Thr	Pro	
				335					340					345	
Tyr	Phe	Pro	Ser	Tyr	Tyr	Ser	Pro	Gln	Thr	His	Cys	Ser	Trp	His	
				350					355					360	
Leu	Thr	Val	Pro	Ser	Leu	Asp	Tyr	Gly	Leu	Ala	Leu	Trp	Phe	Asp	
				365					370					375	
Ala	Tyr	Ala	Leu	Arg	Arg	Gln	Lys	Tyr	Asp	Leu	Pro	Cys	Thr	Gln	
				380					385					390	
Gly	Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile	
				395					400					405	
Leu	Gln	Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly	
				410					415					420	
Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly	
				425					430					435	
Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro	
				440					445					450	
Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys	
				455					460					465	
Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys	
				470					475					480	
Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile	
				485					490					495	
Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly	
				500					505					510	
Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe	
				515					520					525	
Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro	
				530					535					540	
Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu	
				545					550					555	
His	Cys	Asp	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly	
				560					565					570	
Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	
				575					580					585	

Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala Asp	590	595	600
Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met	605	610	615
Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln	620	625	630
Asn Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu	635	640	645
Leu Leu His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val	650	655	660
Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val	665	670	675
Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly	680	685	690
Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly	695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro	710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg	725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln	740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg	755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg	770	775	780
Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser	785	790	795
Trp Ile Gln Gln Val Val Thr	800		

<210> 170
 <211> 1327
 <212> DNA
 <213> Homo sapiens

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 caccatcaac ttcacctccc agatctccct caccggggccc ggtgtgcggg 150
 tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200

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 cccgcatcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250
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 gcaactgcca agcaggggga caagtat 1327

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccactgcttc cagg 24

<210> 172

<211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 172
 taatccagca gtgcaggccg gg 22

 <210> 173
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 173
 atggcctcca cggctgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

 <210> 174
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 174
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 <210> 175
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 <212> DNA
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 aggcaggac acagagtcca ttcac 25

 <210> 176
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 <212> DNA
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 <210> 177
 <211> 1510
 <212> DNA
 <213> Homo sapiens

<400> 177

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ctccagtcct ccagccccctg gccgagagaa gggctctacc ggccgggatt 150
gctggaaaca ccaagaggtg gtttttggtt tttaaaactt ctgtttcttg 200
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tgcatgtcct aggaaaggga atctttacaa aataaacagt gtggaccctt 1450

aataaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

Met	Ser	Asn	Ser	Val	Pro	Leu	Leu	Cys	Phe	Trp	Ser	Leu	Cys	Tyr
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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20					25					30

Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45

Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50					55					60

His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75

Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90

Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95					100					105

Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
				110					115					120

Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
				125					130					135

Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
				140					145					150

Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
				155					160					165

Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn
				170					175					180

Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195

Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210

Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225

Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230					235					240

Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn	
				245					250					255	
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val	
				260					265					270	
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu	
				275					280					285	
Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser	
				290					295					300	
Asn	Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg	
				305					310					315	
Cys	Asn	Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg	
				320					325					330	
Asn	Ser	Lys	Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg	
				335					340					345	
Gly	Asn	Leu	Gln	Ser	Leu	Glu	Cys	Pro							
				350											

<210> 179
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 179
 gtgagcatga gcgagccgctc cac 23

<210> 180
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 180
 gctattacaa cggttcttgc ggcagc 26

<210> 181
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 181
 ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240
 <212> DNA
 <213> Homo sapiens

<400> 182
 cggacgcgtg ggcggacgcg tgggcctggg caagggccgg ggcgccgggc 50
 cgagccacct cttccctcc cccgcttccc tgtcgcgctc cgctggctgg 100
 acgcgctgga ggagtggagc agcaccggc cggccctggg ggctgacagt 150
 cggcaaagtt tggcccgaag aggaagtggc ctcaaaccgc ggcaaggctgc 200
 gaccaggcca gaccaggggc gctcgtgcc tgcgggaggc ctgtaggcga 250
 gggcgcgccc cagtgccgag acccggggct tcaggagccg gcccgggag 300
 agaagagtgc ggcggcggac ggagaaaaca actccaaagt tggcgaaagg 350
 caccgcccct actccgggc tgccgcccgc tccccgccc cagccctggc 400
 atccagagta cgggtcgagc ccgggccatg gagccccct ggggaggcgg 450
 caccaggag cctgggcgcc cggggctccg ccgcgacccc atcgggtaga 500
 ccacagaagc tccgggaccc ttccggcacc tctggacagc ccaggatgct 550
 gttggccacc ctctcctcc tctccttg aggcgctctg gccatccag 600
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 ctcccctgcc aactgcacct ggctcatcct gggcagcaag gaacagactg 750
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gagattgtgc agcagcaggc acccccttcc tacgggcagc tcattgcccc 2050
gggtgccatc ccacctgtag aagactttcc tacagagaat cctaatagata 2100
actcagtgtc gggcaacctg cgttctctgc tacagatctt acgccaggat 2150
atgactccag gaggtggccc aggtgcccgc cgtcgtcagc ggggccgctt 2200
gatgcgacgc ctggtacgcc gtctccgccg ctggggcttg ctccctcgaa 2250
ccaacacccc ggctcgggcc tctgaggcca gatcccaggt cacaccttct 2300
gctgctcccc ttgaggccct agatggtggc acagggtccag cccgtgaggg 2350
cggggcagtg ggtgggcaag atggggagca ggcaccccca ctgcccata 2400
aggctccccct cccatctgct agcacgtctc cagccccac tactgtccct 2450
gaagccccag ggccactgcc ctactgcc cttagagccat cactattgtc 2500
tggagtgggtg caggccctgc gagggcgctt gttgccagc ctggggcccc 2550
caggaccaac ccggagcccc cctggacccc acacagcagt cctggccctg 2600
gaagatgagg acgatgtgct actggtgcca ctggctgagc cgggggtgtg 2650
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ctctactgag gcctctcccc tgggggctct actcatagtg gcacaacctt 2750
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 gccatggcca gacacccag tcccttcacc accacctgct cccacgcca 2950
 ccaccatttg ggtggctggt tttaaaaagt aaagttctta gaggatcata 3000
 ggtctggaca ctccatcctt gccaaacctc tacccaaaag tggccttaag 3050
 caccggaatg ccaattaact agagaccctc cagcccccaa ggggaggatt 3100
 tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150
 ctcaaaaaa gagtgaaca aatgcttcta ttccatagct acggcattgc 3200
 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183
 <211> 713
 <212> PRT
 <213> Homo sapiens

<400> 183
 Met Leu Leu Ala Thr Leu Leu Leu Leu Leu Leu Gly Gly Ala Leu
 1 5 10 15
 Ala His Pro Asp Arg Ile Ile Phe Pro Asn His Ala Cys Glu Asp
 20 25 30
 Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro
 35 40 45
 Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu
 50 55 60
 Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys
 65 70 75
 Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro
 80 85 90
 Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu
 95 100 105
 Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly
 110 115 120
 Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln
 125 130 135
 Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His
 140 145 150
 Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys
 155 160 165
 Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro

	170		175		180
Gly Leu Thr Pro	Arg Pro Val Pro Ser	Leu Pro Cys Asn Val Thr			
	185	190			195
Leu Glu Asp Phe	Tyr Gly Val Phe Ser	Ser Pro Gly Tyr Thr His			
	200	205			210
Leu Ala Ser Val	Ser His Pro Gln Ser	Cys His Trp Leu Leu Asp			
	215	220			225
Pro His Asp Gly	Arg Arg Leu Ala Val	Arg Phe Thr Ala Leu Asp			
	230	235			240
Leu Gly Phe Gly	Asp Ala Val His Val	Tyr Asp Gly Pro Gly Pro			
	245	250			255
Pro Glu Ser Ser	Arg Leu Leu Arg Ser	Leu Thr His Phe Ser Asn			
	260	265			270
Gly Lys Ala Val	Thr Val Glu Thr Leu	Ser Gly Gln Ala Val Val			
	275	280			285
Ser Tyr His Thr	Val Ala Trp Ser Asn	Gly Arg Gly Phe Asn Ala			
	290	295			300
Thr Tyr His Val	Arg Gly Tyr Cys Leu	Pro Trp Asp Arg Pro Cys			
	305	310			315
Gly Leu Gly Ser	Gly Leu Gly Ala Gly	Glu Gly Leu Gly Glu Arg			
	320	325			330
Cys Tyr Ser Glu	Ala Gln Arg Cys Asp	Gly Ser Trp Asp Cys Ala			
	335	340			345
Asp Gly Thr Asp	Glu Glu Asp Cys Pro	Gly Cys Pro Pro Gly His			
	350	355			360
Phe Pro Cys Gly	Ala Ala Gly Thr Ser	Gly Ala Thr Ala Cys Tyr			
	365	370			375
Leu Pro Ala Asp	Arg Cys Asn Tyr Gln	Thr Phe Cys Ala Asp Gly			
	380	385			390
Ala Asp Glu Arg	Arg Cys Arg His Cys	Gln Pro Gly Asn Phe Arg			
	395	400			405
Cys Arg Asp Glu	Lys Cys Val Tyr Glu	Thr Trp Val Cys Asp Gly			
	410	415			420
Gln Pro Asp Cys	Ala Asp Gly Ser Asp	Glu Trp Asp Cys Ser Tyr			
	425	430			435
Val Leu Pro Arg	Lys Val Ile Thr Ala	Ala Val Ile Gly Ser Leu			
	440	445			450
Val Cys Gly Leu	Leu Leu Val Ile Ala	Leu Gly Cys Thr Cys Lys			
	455	460			465

Leu	Tyr	Ala	Ile	Arg	Thr	Gln	Glu	Tyr	Ser	Ile	Phe	Ala	Pro	Leu
				470					475					480
Ser	Arg	Met	Glu	Ala	Glu	Ile	Val	Gln	Gln	Gln	Ala	Pro	Pro	Ser
				485					490					495
Tyr	Gly	Gln	Leu	Ile	Ala	Gln	Gly	Ala	Ile	Pro	Pro	Val	Glu	Asp
				500					505					510
Phe	Pro	Thr	Glu	Asn	Pro	Asn	Asp	Asn	Ser	Val	Leu	Gly	Asn	Leu
				515					520					525
Arg	Ser	Leu	Leu	Gln	Ile	Leu	Arg	Gln	Asp	Met	Thr	Pro	Gly	Gly
				530					535					540
Gly	Pro	Gly	Ala	Arg	Arg	Arg	Gln	Arg	Gly	Arg	Leu	Met	Arg	Arg
				545					550					555
Leu	Val	Arg	Arg	Leu	Arg	Arg	Trp	Gly	Leu	Leu	Pro	Arg	Thr	Asn
				560					565					570
Thr	Pro	Ala	Arg	Ala	Ser	Glu	Ala	Arg	Ser	Gln	Val	Thr	Pro	Ser
				575					580					585
Ala	Ala	Pro	Leu	Glu	Ala	Leu	Asp	Gly	Gly	Thr	Gly	Pro	Ala	Arg
				590					595					600
Glu	Gly	Gly	Ala	Val	Gly	Gly	Gln	Asp	Gly	Glu	Gln	Ala	Pro	Pro
				605					610					615
Leu	Pro	Ile	Lys	Ala	Pro	Leu	Pro	Ser	Ala	Ser	Thr	Ser	Pro	Ala
				620					625					630
Pro	Thr	Thr	Val	Pro	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Ser	Leu	Pro
				635					640					645
Leu	Glu	Pro	Ser	Leu	Leu	Ser	Gly	Val	Val	Gln	Ala	Leu	Arg	Gly
				650					655					660
Arg	Leu	Leu	Pro	Ser	Leu	Gly	Pro	Pro	Gly	Pro	Thr	Arg	Ser	Pro
				665					670					675
Pro	Gly	Pro	His	Thr	Ala	Val	Leu	Ala	Leu	Glu	Asp	Glu	Asp	Asp
				680					685					690
Val	Leu	Leu	Val	Pro	Leu	Ala	Glu	Pro	Gly	Val	Trp	Val	Ala	Glu
				695					700					705
Ala	Glu	Asp	Glu	Pro	Leu	Leu	Thr							
				710										

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcaaggtcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtccca ctc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgcctgctgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100
gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150

aataaaacat cgcccccttct gcttcagtgt gaaaggccac gtgaagatgc 200
 tgcggctggc actaactgtg acatctatga ccttttttat catcgacaaa 250
 gccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300
 atttttcata cttttatatg tactcagact tgatcgatta atgaagtggg 350
 tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400
 atgctcatcg tatctgtgtt ggcaactgata ccagaaacca caacattgac 450
 agttgggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500
 acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550
 cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600
 tttttagttt gataactaagt attaaacata tttctgtatt cttccaaaaa 650
 aaaaaaaaaa aaa 663

<210> 190
 <211> 152
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe
 1 5 10 15
 Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val
 20 25 30
 Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr
 35 40 45
 Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile
 50 55 60
 Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe
 65 70 75
 Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe
 80 85 90
 Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
 95 100 105
 Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys
 110 115 120
 Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn
 125 130 135
 Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
 140 145 150

Val Leu

<210> 191
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 212, 234, 487
<223> unknown base

<400> 191
gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgctatcg 50
ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100
ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150
catcgcccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200
ggcactaaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350
gcctttgctt gatattatca actcactggt aacaacagta ttcattgctca 400
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cgttttgcag aacctactca ggcag 25

<210> 193
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 193
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194
<211> 40

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 194
aaagtgctgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195
<211> 1879
<212> DNA
<213> Homo sapien

<400> 195
cagccccgcg cgccggccga gtcgctgagc cgcggtgcc ggacgggacg 50
ggaccggcta ggctggggcg gccccccggg ccccgccgtg ggcatgggag 100
cactggcccc ggcgctgctg ctgcctctgc tggcccagtg gctcctgcgc 150
gccgcccccg agctggcccc cgcgcccttc acgtgcccc tccgggtggc 200
cgcgcccacg aaccgcgtag ttgcgccac cccgggaccc gggacccttg 250
ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgccctggcg 300
tcccccgcg ggcgcgcaa cttcttgcc atggtagaca acctgcaggg 350
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ggaacccgc actcctacat agacacgtac ttgacacag agaggtctag 500
cacataccgc tccaagggct ttgacgtcac agtgaagtac acacaaggaa 550
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aatacttctt ttcttgtaa cattgccact atttttgaat cagagaattt 650
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cttgcccgtt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850
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gaagagtggg actaccagat agaaattctg aaattggaaa ttggaggcca 950
aagccttaat ctggactgca gagagtataa cgagacaag gccatcgtgg 1000
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 tcattccgta tcacaatcct gcctcagctt tacattcagc ccatgatggg 1250
 ggccggcctg aattatgaat gttaccgatt cggcatttcc ccatccacaa 1300
 atgcgctggg gatcggtgcc acggtgatgg agggcttcta cgtcatcttc 1350
 gacagagccc agaagagggg gggcttcgca gcgagcccct gtgcagaaat 1400
 tgcagggtgct gcagtgtctg aaatttccgg gcctttctca acagaggatg 1450
 tagccagcaa ctgtgtcccc gctcagtctt tgagcgagcc cattttgtgg 1500
 attgtgtcct atgcgctcat gagcgtctgt ggagccatcc tccttgtctt 1550
 aatcgtcctg ctgctgctgc cgttccgggtg tcagcgtcgc ccccgtagcc 1600
 ctgagggtcgt caatgatgag tcctctctgg tcagacatcg ctggaaatga 1650
 atagccaggc ctgacctcaa gcaaccatga actcagctat taagaaaatc 1700
 acatttccag ggcagcagcc gggatcgatg gtggcgcttt ctctgtgcc 1750
 caccgctctt caatctctgt tctgtctcca gatgccttct agattcactg 1800
 tcttttgatt cttgattttc aagctttcaa atcctcccta cttccaagaa 1850
 aaataattaa aaaaaaaact tcattctaa 1879

<210> 196
 <211> 518
 <212> PRT
 <213> Homo sapien

<400> 196
 Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln
 1 5 10 15
 Trp Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr
 20 25 30
 Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro
 35 40 45
 Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu
 50 55 60
 Ala Leu Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala
 65 70 75
 Asn Phe Leu Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg
 80 85 90
 Gly Tyr Tyr Leu Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu
 95 100 105

Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly	
				110					115					120	
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser	
				125					130					135	
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr	
				140					145					150	
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile	
				155					160					165	
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile	
				170					175					180	
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly	
				185					190					195	
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser	
				200					205					210	
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro	
				215					220					225	
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala	
				230					235					240	
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu	
				245					250					255	
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu	
				260					265					270	
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly	
				275					280					285	
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala	
				290					295					300	
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val	
				305					310					315	
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro	
				320					325					330	
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp	
				335					340					345	
Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	
				350					355					360	
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	
				365					370					375	
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	
				380					385					390	
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu	

	395		400		405
Val Ile Gly Ala	Thr Val Met Glu Gly	Phe Tyr Val Ile Phe Asp			
	410	415			420
Arg Ala Gln Lys	Arg Val Gly Phe Ala	Ala Ser Pro Cys Ala Glu			
	425	430			435
Ile Ala Gly Ala	Ala Val Ser Glu Ile	Ser Gly Pro Phe Ser Thr			
	440	445			450
Glu Asp Val Ala	Ser Asn Cys Val Pro	Ala Gln Ser Leu Ser Glu			
	455	460			465
Pro Ile Leu Trp	Ile Val Ser Tyr Ala	Leu Met Ser Val Cys Gly			
	470	475			480
Ala Ile Leu Leu	Val Leu Ile Val Leu	Leu Leu Leu Pro Phe Arg			
	485	490			495
Cys Gln Arg Arg	Pro Arg Asp Pro Glu	Val Val Asn Asp Glu Ser			
	500	505			510
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<220>
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 <212> DNA
 <213> Artificial Sequence

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<210> 201
<211> 18
<212> DNA
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<220>
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<400> 201
ggtcctgtgc ctggatgg 18

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<212> DNA
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<210> 203
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<212> DNA
<213> Artificial Sequence

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<213> Homo sapiens

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 <213> Homo sapiens

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 Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly
 50 55 60
 Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala
 65 70 75
 Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile
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 Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe
 95 100 105
 Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile
 110 115 120
 His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe
 125 130 135
 Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr
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Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe
				170					175					180
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg
				185					190					195
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu
				200					205					210
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala
				215					220					225
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro
				230					235					240
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu
				245					250					255
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu
				260					265					270
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys
				275					280					285
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala
				290					295					300
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro
				305					310					315
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser
				320					325					330
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr
				335					340					345
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser
				350					355					360
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<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<211> 985

<212> PRT

<213> Homo sapiens

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Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
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Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
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Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
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His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
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Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
				95					100					105

Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
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Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
				125					130					135

Cys	Gly	Pro	Pro	Trp	Gly	His	Pro	Glu	Pro	Thr	Val	Ser	Trp	Trp
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Lys	Asp	Gly	Lys	Pro	Leu	Ala	Leu	Gln	Pro	Gly	Arg	His	Thr	Val
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Ser	Gly	Gly	Ser	Leu	Leu	Met	Ala	Arg	Ala	Glu	Lys	Ser	Asp	Glu
				170					175					180

Gly	Thr	Tyr	Met	Cys	Val	Ala	Thr	Asn	Ser	Ala	Gly	His	Arg	Glu
				185					190					195

Ser	Arg	Ala	Ala	Arg	Val	Ser	Ile	Gln	Glu	Pro	Gln	Asp	Tyr	Thr
				200					205					210

Glu	Pro	Val	Glu	Leu	Leu	Ala	Val	Arg	Ile	Gln	Leu	Glu	Asn	Val
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Thr	Leu	Leu	Asn	Pro	Asp	Pro	Ala	Glu	Gly	Pro	Lys	Pro	Arg	Pro
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Ala	Val	Trp	Leu	Ser	Trp	Lys	Val	Ser	Gly	Pro	Ala	Ala	Pro	Ala	
				245					250					255	
Gln	Ser	Tyr	Thr	Ala	Leu	Phe	Arg	Thr	Gln	Thr	Ala	Pro	Gly	Gly	
				260					265					270	
Gln	Gly	Ala	Pro	Trp	Ala	Glu	Glu	Leu	Leu	Ala	Gly	Trp	Gln	Ser	
				275					280					285	
Ala	Glu	Leu	Gly	Gly	Leu	His	Trp	Gly	Gln	Asp	Tyr	Glu	Phe	Lys	
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Val	Arg	Pro	Ser	Ser	Gly	Arg	Ala	Arg	Gly	Pro	Asp	Ser	Asn	Val	
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Leu	Leu	Leu	Arg	Leu	Pro	Glu	Lys	Val	Pro	Ser	Ala	Pro	Pro	Gln	
				320					325					330	
Glu	Val	Thr	Leu	Lys	Pro	Gly	Asn	Gly	Thr	Val	Phe	Val	Ser	Trp	
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Val	Pro	Pro	Pro	Ala	Glu	Asn	His	Asn	Gly	Ile	Ile	Arg	Gly	Tyr	
				350					355					360	
Gln	Val	Trp	Ser	Leu	Gly	Asn	Thr	Ser	Leu	Pro	Pro	Ala	Asn	Trp	
				365					370					375	
Thr	Val	Val	Gly	Glu	Gln	Thr	Gln	Leu	Glu	Ile	Ala	Thr	His	Met	
				380					385					390	
Pro	Gly	Ser	Tyr	Cys	Val	Gln	Val	Ala	Ala	Val	Thr	Gly	Ala	Gly	
				395					400					405	
Ala	Gly	Glu	Pro	Ser	Arg	Pro	Val	Cys	Leu	Leu	Leu	Glu	Gln	Ala	
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Met	Glu	Arg	Ala	Thr	Gln	Glu	Pro	Ser	Glu	His	Gly	Pro	Trp	Thr	
				425					430					435	
Leu	Glu	Gln	Leu	Arg	Ala	Thr	Leu	Lys	Arg	Pro	Glu	Val	Ile	Ala	
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Thr	Cys	Gly	Val	Ala	Leu	Trp	Leu	Leu	Leu	Leu	Gly	Thr	Ala	Val	
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Ser	Gly	Ser	Arg	Asp	Leu	Ser	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Arg	
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Leu	Gly	Ala	Asp	Ala	Arg	Asp	Pro	Leu	Asp	Cys	Arg	Arg	Ser	Leu	

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Thr	Pro	Ala	Arg	Pro	Ser	Pro	Gln	Val	Pro	Ala	Val	Arg	Arg	Leu
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Pro	Pro	Gln	Leu	Ala	Gln	Leu	Ser	Ser	Pro	Cys	Ser	Ser	Ser	Asp
				590					595					600
Ser	Leu	Cys	Ser	Arg	Arg	Gly	Leu	Ser	Ser	Pro	Arg	Leu	Ser	Leu
				605					610					615
Ala	Pro	Ala	Glu	Ala	Trp	Lys	Ala	Lys	Lys	Lys	Gln	Glu	Leu	Gln
				620					625					630
His	Ala	Asn	Ser	Ser	Pro	Leu	Leu	Arg	Gly	Ser	His	Ser	Leu	Glu
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Leu	Arg	Ala	Cys	Glu	Leu	Gly	Asn	Arg	Gly	Ser	Lys	Asn	Leu	Ser
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Gln	Ser	Pro	Gly	Ala	Val	Pro	Gln	Ala	Leu	Val	Ala	Trp	Arg	Ala
				665					670					675
Leu	Gly	Pro	Lys	Leu	Leu	Ser	Ser	Ser	Asn	Glu	Leu	Val	Thr	Arg
				680					685					690
His	Leu	Pro	Pro	Ala	Pro	Leu	Phe	Pro	His	Glu	Thr	Pro	Pro	Thr
				695					700					705
Gln	Ser	Gln	Gln	Thr	Gln	Pro	Pro	Val	Ala	Pro	Gln	Ala	Pro	Ser
				710					715					720
Ser	Ile	Leu	Leu	Pro	Ala	Ala	Pro	Ile	Pro	Ile	Leu	Ser	Pro	Cys
				725					730					735
Ser	Pro	Pro	Ser	Pro	Gln	Ala	Ser	Ser	Leu	Ser	Gly	Pro	Ser	Pro
				740					745					750
Ala	Ser	Ser	Arg	Leu	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Leu	Gly	Glu
				755					760					765
Asp	Gln	Asp	Ser	Val	Leu	Thr	Pro	Glu	Glu	Val	Ala	Leu	Cys	Leu
				770					775					780
Glu	Leu	Ser	Glu	Gly	Glu	Glu	Thr	Pro	Arg	Asn	Ser	Val	Ser	Pro
				785					790					795
Met	Pro	Arg	Ala	Pro	Ser	Pro	Pro	Thr	Thr	Tyr	Gly	Tyr	Ile	Ser
				800					805					810
Val	Pro	Thr	Ala	Ser	Glu	Phe	Thr	Asp	Met	Gly	Arg	Thr	Gly	Gly
				815					820					825

Gly	Val	Gly	Pro	Lys	Gly	Gly	Val	Leu	Leu	Cys	Pro	Pro	Arg	Pro	
				830					835					840	
Cys	Leu	Thr	Pro	Thr	Pro	Ser	Glu	Gly	Ser	Leu	Ala	Asn	Gly	Trp	
				845					850					855	
Gly	Ser	Ala	Ser	Glu	Asp	Asn	Ala	Ala	Ser	Ala	Arg	Ala	Ser	Leu	
				860					865					870	
Val	Ser	Ser	Ser	Asp	Gly	Ser	Phe	Leu	Ala	Asp	Ala	His	Phe	Ala	
				875					880					885	
Arg	Ala	Leu	Ala	Val	Ala	Val	Asp	Ser	Phe	Gly	Phe	Gly	Leu	Glu	
				890					895					900	
Pro	Arg	Glu	Ala	Asp	Cys	Val	Phe	Ile	Asp	Ala	Ser	Ser	Pro	Pro	
				905					910					915	
Ser	Pro	Arg	Asp	Glu	Ile	Phe	Leu	Thr	Pro	Asn	Leu	Ser	Leu	Pro	
				920					925					930	
Leu	Trp	Glu	Trp	Arg	Pro	Asp	Trp	Leu	Glu	Asp	Met	Glu	Val	Ser	
				935					940					945	
His	Thr	Gln	Arg	Leu	Gly	Arg	Gly	Met	Pro	Pro	Trp	Pro	Pro	Asp	
				950					955					960	
Ser	Gln	Ile	Ser	Ser	Gln	Arg	Ser	Gln	Leu	His	Cys	Arg	Met	Pro	
				965					970					975	
Lys	Ala	Gly	Ala	Ser	Pro	Val	Asp	Tyr	Ser						
				980					985						

<210> 212
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 212
 gaagggacct acatgtgtgt ggcc 24

<210> 213
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 213
 actgaccttc cagctgagcc acac 24

<210> 214
 <211> 50
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 214

aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

ctcccacggt gtccagcgcc cagaatgcgg cttctggtcc tgctatgggg 50

ttgcctgctg ctcccaggtt atgaagccct ggagggccca gaggaatca 100

gcgggttcga aggggacact gtgtccctgc agtgcaccta caggaagag 150

ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200

tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcaggggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtgggg 350

cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtctttc 400

caggaccctg ctgtccctcc tcccttctc ccaccttcca gcctctgggt 450

acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccagg 500

attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550

agacaggggc tgaggcccct ccattgccag ggacttcca gtacgggcac 600

gaaaggactt ctgagtacac aggaacctct cctcaccag cgacctctcc 650

tcctgcaggg agtcccgcc ccccatgca gctggactcc acctcagcag 700

aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750

atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800

gtcagcgcga ggctgatcg ccttctgcag ccacctgctc ctgtggagaa 850

aggaagctca acaggccacg gagacacaga ggaacgagaa gttctggctc 900

tcacgcttga ctgcggagga aaaggaagcc ccttcccagg cccctgaggg 950

ggacgtgatc tcgatgcctc cctccacac atctgaggag gagctgggct 1000

tctcgaagtt tgtctcagcg tagggcagga ggcctcctg gccaggccag 1050
cagtgaagca gtatggctgg ctggatcagc accgattccc gaaagctttc 1100
cacctcagcc tcagagtcca gctgcccgga ctccagggtt ctccccaccc 1150
tccccaggct ctctctttgc atgttccagc ctgacctaga agcgtttgtc 1200
agccctggag cccagagcgg tggccttgct cttccggctg gagactggga 1250
catccctgat aggttcacat ccctgggagc agtaccaggc tgctgaccct 1300
cagcagggcc agacaaggct cagtggatct ggtctgagtt tcaatctgcc 1350
aggaactcct gggcctcatg cccagtgtcg gaccctgcct tcctcccact 1400
ccagacccca ccttgtcttc cctccctggc gtcctcagac ttagtcccac 1450
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ggattctggc ttctctttga accacctgca tccagccctt caggaaagcct 1550
gtgaaaaacg tgattcctgg cccaccaag acccaccaa accatctctg 1600
ggcttggtgc aggactctga attctaaca tgcccagtga ctgtcgact 1650
tgagtttgag ggccagtggg cctgatgaac gtcacacccc cttcagctta 1700
gagtctgcat ttgggctgtg acgtctccac ctgcccgaat agatctgctc 1750
tgtctgcgac accagatcca cgtggggact cccctgaggc ctgctaagtc 1800
caggccttgg tcaggtcagg tgcacattgc aggataagcc caggaccggc 1850
acagaagtgg ttgcctttnc catttgccct ccctggncca tgccttcttg 1900
cctttggaaa aaatgatgaa gaaaacctg gtccttcct tgtctggaaa 1950
gggttacttg cctatgggtt ctgggtggcta gagagaaaag tagaaaacca 2000
gagtgcacgt aggtgtctaa cacagaggag agtaggaaca gggcggatac 2050
ctgaagggtga ctccaggtcc agccccctgg agaaggggtc gggggtggtg 2100
gtaaagtagc acaactacta tttttttct ttttccatta ttattgtttt 2150
ttaagacaga atctcgtgct gctgcccagg ctggagtga gtggcacgat 2200
ctgcaaactc cgctcctgg gttcaagtga ttcttctgcc tcagcctccc 2250
gagtagctgg gattacaggc acgcaccacc acacctggct aatttttgta 2300
cttttagtag agatgggggt tcaacctggt ggccaggctg gtcttgaact 2350
cctgacctca aatgagctc ctgcttcagt ctcccaaatt gccgggatta 2400
caggcatgag ccactgtgtc tggccctatt tcctttaaaa agtgaaatta 2450

agagttgttc agtatgcaaa acttggaaa atggaggaga aaaagaaaag 2500
gaagaaaaaa atgtcaccca tagtctcacc agagactatc attatttcgt 2550
tttgtgttac ttccttccac tcttttcttc ttcacataat ttgccggtgt 2600
tctttttaca gagcaattat cttgtatata caactttgta tcctgccttt 2650
tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700
gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaa 2749

<210> 216
<211> 332
<212> PRT
<213> Homo sapiens

<400> 216
Met Arg Leu Leu Val Leu Leu Trp Gly Cys Leu Leu Leu Pro Gly
1 5 10 15
Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly
20 25 30
Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp
35 40 45
His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg
50 55 60
Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met
65 70 75
Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu
80 85 90
Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr
95 100 105
Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile
110 115 120
Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser
125 130 135
Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala
140 145 150
Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu
155 160 165
Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu
170 175 180
Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr
185 190 195
Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro

	200	205	210
Ala Gly Ser Ser	Arg Pro Pro Met Gln	Leu Asp Ser Thr Ser	Ala
	215	220	225
Glu Asp Thr Ser	Pro Ala Leu Ser Ser	Gly Ser Ser Lys Pro	Arg
	230	235	240
Val Ser Ile Pro	Met Val Arg Ile Leu	Ala Pro Val Leu Val	Leu
	245	250	255
Leu Ser Leu Leu	Ser Ala Ala Gly Leu	Ile Ala Phe Cys Ser	His
	260	265	270
Leu Leu Leu Trp	Arg Lys Glu Ala Gln	Gln Ala Thr Glu Thr	Gln
	275	280	285
Arg Asn Glu Lys	Phe Trp Leu Ser Arg	Leu Thr Ala Glu Glu	Lys
	290	295	300
Glu Ala Pro Ser	Gln Ala Pro Glu Gly	Asp Val Ile Ser Met	Pro
	305	310	315
Pro Leu His Thr	Ser Glu Glu Glu Leu	Gly Phe Ser Lys Phe	Val
	320	325	330
Ser Ala			

<210> 217
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 217
 ccctgcagtg cacctacagg gaag 24

<210> 218
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 218
 ctgtcttccc ctgcttggct gtgg 24

<210> 219
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

09978187 "101501

<400> 219
gggtgcaggaa gggtgggatc ctcttctctc gctgctctgg ccacatc 47

<210> 220
<211> 950
<212> DNA
<213> Homo sapiens

<400> 220
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50
ggggtggcag gagccgcaga gccagagcag acagccgaga aacagggtga 100
cagtgtgaaa gaaccagtgg tctcgtctctg ttgccagggc tagagtgtac 150
tggcgtgatc atagctcact gcagcctcag actcctggac ttgagaaatc 200
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250
cctgtttctt ctcttctgt gagtggacca cggaggctgg tgagctgcct 300
gtcatcccaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350
ccgccggcat agaagccagg agcagggctc tcagaaggcg gtggtgcca 400
gctgggatca tgttgttggc cctggctctgt ctgctcagct gcctgctacc 450
ctccagttag gccaaagctct acggctcgtt tgaaactggcc agagtgtac 500
atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550
tgcttgcctt atttcacaag cggtttcaac gcagctgctt tggactacga 600
ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggagggt 650
ggtgcagcaa cctcaccocg aacgtcccca acgtgtgccg gatgtactgc 700
tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750
gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850
gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900
cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221
<211> 146
<212> PRT
<213> Homo sapiens

<400> 221
Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser
1 5 10 15
Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu
20 25 30

His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp
 35 40 45
 Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala
 50 55 60
 Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln
 65 70 75
 Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro
 80 85 90
 Asn Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu
 95 100 105
 Lys Asp Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln
 110 115 120
 Gly Leu Gly Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys
 125 130 135
 Asp Leu Thr Glu Trp Val Asp Gly Cys Asp Phe
 140 145

<210> 222
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 222
 gggatcatgt tgttggccct ggctc 24

<210> 223
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 223
 gcaaggcaga cccagtcagc cag 23

<210> 224
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 224
 ctgcctgcta ccctccaagt gaggccaagc tctacggctg ttgtg 45

<210> 225

<211> 2049
 <212> DNA
 <213> Homo sapiens

<400> 225
 agccgctgcc ccggggccggg cggccgcggc ggcaccatga gtccccgctc 50
 gtgcctgcgt tcgctgcgcc tcctcgtctt cgccgtcttc tcagccgccg 100
 cgagcaactg gctgtacctg gccaaagctgt cgtcgggtggg gagcatctca 150
 gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcagggtgca 200
 gatgtgcaag cggaacctgg aagtcattga ctccgtgcgc cgcggtgccc 250
 agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300
 tgctccacac tcgactcctt gcccgctctt ggcaagggtg tgacgcaagg 350
 gactcgggag gcggccttcg tgtacgccat ctcttcggca ggtgtggcct 400
 ttgcagtgcg gcgggctgac agcagtgggg agctggagaa gtgcggctgt 450
 gacaggacag tgcattgggt cagccacag ggcttcaggt ggtcaggatg 500
 ctctgacaac atcgctacg gtgtggcctt ctacagtcg tttgtggatg 550
 tgccgggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600
 cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650
 atgcaagtgc cacggggtgt caggtcctctg tgaggtaaag acgtgctggc 700
 gagccgtgcc gcccttcgc cagggtgggtc acgcactgaa ggagaagttt 750
 gatggtgcca ctgagggtga gccacgccgc gtgggctcct ccagggcact 800
 ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850
 acttgagacc tagccccgac ttctgtgagc aggacatgcg cagcggcgtg 900
 ctgggcacga ggggccgcac atgcaacaag acgtccaagg ccatcgacgg 950
 ctgtgagctg ctgtgctgtg gccgcggctt ccacacggcg cagggtggagc 1000
 tggctgaacg ctgcagctgc aaattccact ggtgctgctt cgtcaagtgc 1050
 cggcagtgcc agcggctcgt ggagttgcac acgtgccgat gaccgcctgc 1100
 ctagccctgc gccggcaacc acctagtggc ccagggaagg ccgataattt 1150
 aaacagtctc ccaccaccta cccaagaga tactggttgt attttttgtt 1200
 ctggttttgt ttttgggtcc tcatgttatt tattgccgaa accaggcagg 1250
 caacccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300
 ctgccactga ccaaaggac cttgctcgtg ccgctggctg cccgcatgtg 1350

gctgccactg accactcagt tggtatctgt gtccgttttt ctacttgcag 1400
 acctaaggtg gagtaacaag gagtattacc accacatggc tactgaccgt 1450
 gtcacatgggg aagagggggc cttatggcag ggaaaatagg taccgacttg 1500
 atggaagtca caccctctgg aaaaaagaac tcttaactct ccagcacaca 1550
 tacacatgga ctcttggcag cttgagccta gaagccatgt ctctcaaagt 1600
 ccctgagaaa gggaacaagc agataccagg tcaagggcac caggttcatt 1650
 tcagccctta catggacagc tagaggttcg atatctgtgg gtccttccag 1700
 gcaagaagag ggagatgaga gcaagagacg actgaagtcc caccctagaa 1750
 cccagcctgc cccagcctgc ccctgggaag aggaaactta accactcccc 1800
 agaccacact aggcaggcat ataggctgcc atcctggacc agggatcccc 1850
 gctgtgcctt tgcagtcatg cccgagtcac ctttcacagc gctgttcctc 1900
 catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950
 acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000
 ctgtgccttt gcagtcatgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226
 <211> 351
 <212> PRT
 <213> Homo sapiens

<400> 226
 Met Ser Pro Arg Ser Cys Leu Arg Ser Leu Arg Leu Leu Val Phe
 1 5 10 15
 Ala Val Phe Ser Ala Ala Ala Ser Asn Trp Leu Tyr Leu Ala Lys
 20 25 30
 Leu Ser Ser Val Gly Ser Ile Ser Glu Glu Glu Thr Cys Glu Lys
 35 40 45
 Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn
 50 55 60
 Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile
 65 70 75
 Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser
 80 85 90
 Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly
 95 100 105
 Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val
 110 115 120

Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys
				125					130					135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe
				140					145					150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe
				155					160					165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser
				170					175					180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg
				185					190					195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly
				200					205					210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro
				215					220					225
Pro	Phe	Arg	Gln	Val	Gly	His	Ala	Leu	Lys	Glu	Lys	Phe	Asp	Gly
				230					235					240
Ala	Thr	Glu	Val	Glu	Pro	Arg	Arg	Val	Gly	Ser	Ser	Arg	Ala	Leu
				245					250					255
Val	Pro	Arg	Asn	Ala	Gln	Phe	Lys	Pro	His	Thr	Asp	Glu	Asp	Leu
				260					265					270
Val	Tyr	Leu	Glu	Pro	Ser	Pro	Asp	Phe	Cys	Glu	Gln	Asp	Met	Arg
				275					280					285
Ser	Gly	Val	Leu	Gly	Thr	Arg	Gly	Arg	Thr	Cys	Asn	Lys	Thr	Ser
				290					295					300
Lys	Ala	Ile	Asp	Gly	Cys	Glu	Leu	Leu	Cys	Cys	Gly	Arg	Gly	Phe
				305					310					315
His	Thr	Ala	Gln	Val	Glu	Leu	Ala	Glu	Arg	Cys	Ser	Cys	Lys	Phe
				320					325					330
His	Trp	Cys	Cys	Phe	Val	Lys	Cys	Arg	Gln	Cys	Gln	Arg	Leu	Val
				335					340					345
Glu	Leu	His	Thr	Cys	Arg									
				350										

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 228
tgggtgggaga ctgttttaaata taccggcc 28

<210> 229
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 229
tgcttcgtca agtgccggca gtgccagcgg ctctgtggagt t 41

<210> 230
<211> 1355
<212> DNA
<213> Homo sapiens

<400> 230
cggacgcgtg ggcggacgcg tgggcggacg cgtgggcgga cgcgtgggct 50
gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100
gctccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200
ggctgtgatt ctgagtatcc tattgtccaa ggccctccag gacgcgcgg 250
cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300
gcggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350
ctcggggacg caggcgcagc tgcagaccac gcgcgcggag ctgggggagg 400
cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450
cgcgtgaccc agggcttggc tgaagccggc aggggcccgtg aggacgtccg 500
cactgagctg ttccgggcgc tggaggccgt gaggtccag aacaactcct 550
gcgagccgtg cccacgctg tggctgtcct tcgagggtc ctgctacttt 600
ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650
tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggttcc 700
tcaactcgaa cacgcgtggc cgtggttact ggctgggcct gagggtgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800
cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850
agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950
ccgcccagtg ccctggagcc gcgcccattg cagcatgtcg tatcctgggg 1000
gctgctcacc tccctggctc ctggagctga ttgccaaaga gtttttttct 1050
tcctcatcca ccgctgctga gtctcagaaa cacttggccc aacatagccc 1100
tgtccagccc agtgccctggg ctctgggacc tccatgccga cctcatccta 1150
actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200
ctcctgcgtc cccgtgatat gcctccactt ctctccctaa ccaagggttag 1250
gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300
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aaaaa 1355

<210> 231
<211> 293
<212> PRT
<213> Homo sapiens

<400> 231
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1 5 10 15
Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg
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Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp
35 40 45
Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg
50 55 60
Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser
65 70 75
Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp
80 85 90
Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr
95 100 105
Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu
110 115 120
Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala
125 130 135

Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	
				140					145					150	
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	
				155					160					165	
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	
				170					175					180	
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	
				185					190					195	
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	
				200					205					210	
Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu	
				215					220					225	
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val	
				230					235					240	
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro	
				245					250					255	
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr	
				260					265					270	
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp	
				275					280					285	
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys								
				290											

<210> 232
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 232
 gcgagaactg tgtcatgatg ctgc 24

<210> 233
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 233
 gtttctgaga ctcagcagcg gtgg 24

<210> 234
 <211> 50
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

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ctccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150

agacaggagg aactggagcc tcattggccg gcccgggcg cgggcctcgg 200

gcttaaataag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250

cgctcccgt gctcctgccg ggtgatggaa aacccagcc cggccgccgc 300

cctgggcaag gccctctgcg ctctcctcct ggccactctc ggccgccgcg 350

gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400

tacagcatca cttcacggg caagtggagc cagacggcct tccccagca 450

gtaccccctg ttccgcccc ctgcgcagtg gtcttcgctg ctgggggccg 500

cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550

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cgcccgccgt cccagcggc accgggcaga cgtcggcgga gctggaggtg 700

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ggtgaccgag ataacgtcct cctctcccag ccaccggcc aactccttct 950

actaccgcg gctgaaggcc ctgcctccca tcgccagggt gacactgctg 1000

cggctgcgac agagcccag ggccttcac cctcccgcc cagtctgcc 1050

cagcagggac aatgagattg tagacagcgc ctcaattcca gaaacgccgc 1100

tggactgcga ggtctccctg tggctcgtcct ggggactgtg cggaggccac 1150
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 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

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				20					25					30
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile
				35					40					45
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr
				50					55					60
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala
				65					70					75
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val
				80					85					90
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala
				95					100					105
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val

	110		115		120
His Glu Val Phe	Ser Ala Pro Ala Val	Pro Ser Gly Thr Gly	Gln		
	125	130	135		
Thr Ser Ala Glu	Leu Glu Val Gln Arg	Arg His Ser Leu Val	Ser		
	140	145	150		
Phe Val Val Arg	Ile Val Pro Ser Pro	Asp Trp Phe Val Gly	Val		
	155	160	165		
Asp Ser Leu Asp	Leu Cys Asp Gly Asp	Arg Trp Arg Glu Gln	Ala		
	170	175	180		
Ala Leu Asp Leu	Tyr Pro Tyr Asp Ala	Gly Thr Asp Ser Gly	Phe		
	185	190	195		
Thr Phe Ser Ser	Pro Asn Phe Ala Thr	Ile Pro Gln Asp Thr	Val		
	200	205	210		
Thr Glu Ile Thr	Ser Ser Ser Pro Ser	His Pro Ala Asn Ser	Phe		
	215	220	225		
Tyr Tyr Pro Arg	Leu Lys Ala Leu Pro	Pro Ile Ala Arg Val	Thr		
	230	235	240		
Leu Leu Arg Leu	Arg Gln Ser Pro Arg	Ala Phe Ile Pro Pro	Ala		
	245	250	255		
Pro Val Leu Pro	Ser Arg Asp Asn Glu	Ile Val Asp Ser Ala	Ser		
	260	265	270		
Val Pro Glu Thr	Pro Leu Asp Cys Glu	Val Ser Leu Trp Ser	Ser		
	275	280	285		
Trp Gly Leu Cys	Gly Gly His Cys Gly	Arg Leu Gly Thr Lys	Ser		
	290	295	300		
Arg Thr Arg Tyr	Val Arg Val Gln Pro	Ala Asn Asn Gly Ser	Pro		
	305	310	315		
Cys Pro Glu Leu	Glu Glu Glu Ala Glu	Cys Val Pro Asp Asn	Cys		
	320	325	330		

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcactgcc aggggaagag gg 22

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<210> 238
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 238
caggactcgc tacgtccg 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
cagccccttc tcctcctttc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
gcagttatca gggacgcact cagcc 25

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ccagcgagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cggtcaccgt gtcctgcggg atg 23

<210> 243
<211> 42
<212> DNA

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 243

cagcccccttc tccctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

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aggaagagtg tactcgtagg cggacagctt tagtggccgg ccggccgctc 150
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg 300
cagaaatttt atccaacttt gtttggaagc ttattatgac aataccattt 350
ttcatagagt tgtgcctggt ttcatagtcc aaggcggaga tcctactggc 400
acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450
tcattcacgg ttgcgtttta atcggagagg actggttgcc atggcaaagt 500
ctggtttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550
gatgaactta acaataagca taccatcttt ggaaagggtta caggggatac 600
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gaccacataa tccacacaaa ataaaaagct gtgagggtttt gtttaatcct 700
tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaacc 750
agaggaggaa gtaaagaaat tgaaacccaa aggcacaaaa aatttttagtt 800
tactttcatt tggagaggaa gctgaggaag aagaggagga agtaaatacga 850
gttagtcaga gcatgaaggc caaaagcaaa agtagtcatg acttgcttaa 900
ggatgatcca catctcagtt ctgttccagt tgtagaaagt gaaaaagggtg 950
atgcaccaga tttagttgat gatggagaag atgaaagtgc agagcatgat 1000
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aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150
agacaattaa aacgggaact cttagcagca aaacaaaaaa aagtagaaaa 1200
tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gcccctccag 1250
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tcacatgtac ttcagtttga ggataaaagc agaaaagtga aagatgcaag 1500
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agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1650
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catgtgtttt ttcctagctg acctttttata ttgctaaatc tgaaataaaa 1850
taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245
<211> 472
<212> PRT
<213> Homo sapiens

<400> 245
Met Ser Asn Ile Tyr Ile Gln Glu Pro Pro Thr Asn Gly Lys Val
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Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser
20 25 30
Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu
35 40 45
Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly
50 55 60
Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly
65 70 75
Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg
80 85 90
Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly
95 100 105

Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala	110	115	120
Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly	125	130	135
Asp	Thr	Val	Tyr	Asn	Met	Leu	Arg	Leu	Ser	Glu	Val	Asp	Ile	Asp	140	145	150
Asp	Asp	Glu	Arg	Pro	His	Asn	Pro	His	Lys	Ile	Lys	Ser	Cys	Glu	155	160	165
Val	Leu	Phe	Asn	Pro	Phe	Asp	Asp	Ile	Ile	Pro	Arg	Glu	Ile	Lys	170	175	180
Arg	Leu	Lys	Lys	Glu	Lys	Pro	Glu	Glu	Glu	Val	Lys	Lys	Leu	Lys	185	190	195
Pro	Lys	Gly	Thr	Lys	Asn	Phe	Ser	Leu	Leu	Ser	Phe	Gly	Glu	Glu	200	205	210
Ala	Glu	Glu	Glu	Glu	Glu	Glu	Val	Asn	Arg	Val	Ser	Gln	Ser	Met	215	220	225
Lys	Gly	Lys	Ser	Lys	Ser	Ser	His	Asp	Leu	Leu	Lys	Asp	Asp	Pro	230	235	240
His	Leu	Ser	Ser	Val	Pro	Val	Val	Glu	Ser	Glu	Lys	Gly	Asp	Ala	245	250	255
Pro	Asp	Leu	Val	Asp	Asp	Gly	Glu	Asp	Glu	Ser	Ala	Glu	His	Asp	260	265	270
Glu	Tyr	Ile	Asp	Gly	Asp	Glu	Lys	Asn	Leu	Met	Arg	Glu	Arg	Ile	275	280	285
Ala	Lys	Lys	Leu	Lys	Lys	Asp	Thr	Ser	Ala	Asn	Val	Lys	Ser	Ala	290	295	300
Gly	Glu	Gly	Glu	Val	Glu	Lys	Lys	Ser	Val	Ser	Arg	Ser	Glu	Glu	305	310	315
Leu	Arg	Lys	Glu	Ala	Arg	Gln	Leu	Lys	Arg	Glu	Leu	Leu	Ala	Ala	320	325	330
Lys	Gln	Lys	Lys	Val	Glu	Asn	Ala	Ala	Lys	Gln	Ala	Glu	Lys	Arg	335	340	345
Ser	Glu	Glu	Glu	Glu	Ala	Pro	Pro	Asp	Gly	Ala	Val	Ala	Glu	Tyr	350	355	360
Arg	Arg	Glu	Lys	Gln	Lys	Tyr	Glu	Ala	Leu	Arg	Lys	Gln	Gln	Ser	365	370	375
Lys	Lys	Gly	Thr	Ser	Arg	Glu	Asp	Gln	Thr	Leu	Ala	Leu	Leu	Asn	380	385	390
Gln	Phe	Lys	Ser	Lys	Leu	Thr	Gln	Ala	Ile	Ala	Glu	Thr	Pro	Glu			

	395		400		405
Asn Asp Ile Pro	Glu Thr Glu Val Glu	Asp Asp Glu Gly Trp	Met		
	410	415	420		
Ser His Val Leu	Gln Phe Glu Asp Lys	Ser Arg Lys Val Lys	Asp		
	425	430	435		
Ala Ser Met Gln	Asp Ser Asp Thr Phe	Glu Ile Tyr Asp Pro	Arg		
	440	445	450		
Asn Pro Val Asn	Lys Arg Arg Arg Glu	Glu Ser Lys Lys Leu	Met		
	455	460	465		
Arg Glu Lys Lys	Glu Arg Arg				
	470				

<210> 246
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 246
 tgcggagatc ctactggcac aggg 24

<210> 247
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 247
 cgagtttagtc agagcatg 18

<210> 248
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<400> 248
 cagatggtgc tggtgccg 18

<210> 249
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 <212> DNA
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<400> 249
caactggaac aggaactgag atgtggatc 29

<210> 250

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 250

ctggttcagc agtgcaaggg tctg 24

<210> 251

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 251

cctctccgat taaaacgc 18

<210> 252

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 252

gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253

<211> 2456

<212> DNA

<213> Homo sapiens

<400> 253

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catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150

ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgccggcgg 200

gaccagcaca ggcggcggtt tctccttcgg aacgggaacg tctagcaacc 250

cttctgtggg gctcaatttt ggaaatcttg gaagtacttc aactccagca 300

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acctgccact gggttcactc taggaggaac aaatacaggt gccttgca 400

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gtctatacac aggggtggtc tcttcaataa agaagtgttg attagaaaaa 2450
aaaaaa 2456

<210> 254
<211> 545
<212> PRT
<213> Homo sapiens

<400> 254
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Thr Val Ala Ala Gly Gly Thr Ser Thr Gly Gly Val Phe Ser Phe
20 25 30
Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly
35 40 45
Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser
50 55 60
Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly
65 70 75
Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg
80 85 90
Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
95 100 105
His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe
110 115 120
Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro
125 130 135

Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	140	145	150
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	155	160	165
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	170	175	180
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	185	190	195
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	200	205	210
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	215	220	225
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	230	235	240
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	245	250	255
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	260	265	270
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	275	280	285
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	290	295	300
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	305	310	315
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	320	325	330
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	335	340	345
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	350	355	360
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	365	370	375
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	380	385	390
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	395	400	405
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	410	415	420
Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp	Asp	Pro			

	425		430		435
Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu	440		445		450
Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn	455		460		465
Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp	470		475		480
Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met	485		490		495
Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr	500		505		510
Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala	515		520		525
Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu	530		535		540
Pro Gln Glu Trp Ala	545				

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 255
 aggtgcctgc aggagtcctg ggg 23

<210> 256
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 256
 ccacctcagg aagccgaaga tgcc 24

<210> 257
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 257
 gaacggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258
 <211> 2764
 <212> DNA
 <213> Homo sapiens

<400> 258
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 actgccactg ctgctgtcct cgctgctggg cgggtcccag gctatggatg 100
 ggagattctg gatacgagtg caggagtcat tgatggtgcc ggagggcctg 150
 tgcattctctg tgccctgtct tttctcctac ccccgacaag actggacagg 200
 gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250
 aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300
 acccgggggc gattccagct cactggggat cccgccaagg ggaactgctc 350
 cttggtgata agagacgcgc agatgcagga tgagtcacag tacttctttc 400
 ggggtggagag aggaagctat gtgacatata atttcatgaa cgatgggttc 450
 tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500
 caccgacctc acctgccatg tggacttctc cagaaagggt gtgagcgcac 550
 agaggaccgt ccgactccgt gtggcctatg ccccagaga ccttggtatc 600
 agcatttcac gtgacaacac gccagccctg gagccccagc cccagggaaa 650
 tgtcccatat ctggaagccc aaaaaggcca gttcctgcgg ctctctctgtg 700
 ctgctgacag ccagccccct gccacactga gctgggtcct gcagaacaga 750
 gtctctctct cgctccatcc ctggggccct agaccctggg ggctggagct 800
 gcccgggggtg aaggctgggg attcagggcg ctacacctgc cgagcggaga 850
 acaggcttgg ctcccagcag cgagccctgg acctctctgt gcagtatcct 900
 ccagagaacc tgagagtgat gggttcccaa gcaaacagga cagtcctgga 950
 aaaccttggg aacggcacgt ctctcccagt actggagggc caaagcctgt 1000
 gcctgggtctg tgtcacacac agcagcccc cagccaggct gagctggacc 1050
 cagaggggac aggttctgag cccctcccag cctcagacc ccggggctct 1100
 ggagctgcct cgggttcaag tggagcacga aggagagttc acctgccacg 1150
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 tataagaagg gactcatctc aacggcattc tccaacggag cgtttctggg 1250
 aatcggcatc acggtctctt ttttctctg cctggccctg atcatcatga 1300

agattctacc gaagagacgg actcagacag aaaccccgag gccaggttc 1350
 tcccggcaca gcacgatcct ggattacatc aatgtggtcc cgacggctgg 1400
 ccccttggtc cagaagcgga atcagaaagc cacaccaaac agtcctcgga 1450
 cccctcctcc accaggtgct ccctccccag aatcaaagaa gaaccagaaa 1500
 aagcagtatc agttgcccag tttcccagaa cccaaatcat ccaactcaagc 1550
 cccagaatcc caggagagcc aagaggagct ccattatgcc acgctcaact 1600
 tcccaggcgt cagacccagg cctgaggccc ggatgcccac gggcacccag 1650
 gcggattatg cagaagtcaa gttccaatga gggctcttta ggcttttagga 1700
 ctgggacttc ggctagggag gaaggtagag taagagggttg aagataacag 1750
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 gcctgtaatc ccagcacttt gggagggttg ggtgggcaga tcgcctgagg 1900
 tcgggagttc gagaccagcc tggccaactt ggtgaaaccc cgtctctact 1950
 aaaaatacaa aaattagctg ggcattggtg caggcgccctg taatcctacc 2000
 tacttgggaa gctgaggcag gagaatcact tgaacctggg agacggagggt 2050
 tgcagtgagc caagatcaca ccattgcacg ccagcctggg caacaaagcg 2100
 agactccatc tcaaaaaaaaa aatcctccaa atggggtggg tgtctgtaat 2150
 cccagcactt tgggaggcta aggtgggtgg attgcttgag cccaggagtt 2200
 cgagaccagc ctgggcaaca tggtgaaacc ccctctctac aaaaaataca 2250
 aaacatagct gggcttggtg gtgtgtgcct gtagtcccag ctgtcagaca 2300
 tttaaaccag agcaactcca tctggaatag gagctgaata aaatgagggt 2350
 gagacctact gggctgcatt ctacagacagt ggaggcattc taagtcacag 2400
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 gccacgagag tgacctctgg tcgtcctcac tgctacactc ctgacagcac 2550
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 cccaaaaggg ggaggaatga ataatccacc ccttggttag caaataagca 2650
 agaaataacc ataaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700
 ctatggagta gccattcttt tgttccttta ctttcttaat aaacttgctt 2750

tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln
1 5 10 15

Ala Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met
20 25 30

Val Pro Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr
35 40 45

Pro Arg Gln Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp
50 55 60

Phe Lys Ala Val Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr
65 70 75

Asn His Gln Ser Arg Glu Val Glu Met Ser Thr Arg Gly Arg Phe
80 85 90

Gln Leu Thr Gly Asp Pro Ala Lys Gly Asn Cys Ser Leu Val Ile
95 100 105

Arg Asp Ala Gln Met Gln Asp Glu Ser Gln Tyr Phe Phe Arg Val
110 115 120

Glu Arg Gly Ser Tyr Val Thr Tyr Asn Phe Met Asn Asp Gly Phe
125 130 135

Phe Leu Lys Val Thr Val Leu Ser Phe Thr Pro Arg Pro Gln Asp
140 145 150

His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly
155 160 165

Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro
170 175 180

Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu
185 190 195

Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys
200 205 210

Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro
215 220 225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser
230 235 240

His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val
245 250 255

Lys	Ala	Gly	Asp	Ser	Gly	Arg	Tyr	Thr	Cys	Arg	Ala	Glu	Asn	Arg	
				260					265					270	
Leu	Gly	Ser	Gln	Gln	Arg	Ala	Leu	Asp	Leu	Ser	Val	Gln	Tyr	Pro	
				275					280					285	
Pro	Glu	Asn	Leu	Arg	Val	Met	Val	Ser	Gln	Ala	Asn	Arg	Thr	Val	
				290					295					300	
Leu	Glu	Asn	Leu	Gly	Asn	Gly	Thr	Ser	Leu	Pro	Val	Leu	Glu	Gly	
				305					310					315	
Gln	Ser	Leu	Cys	Leu	Val	Cys	Val	Thr	His	Ser	Ser	Pro	Pro	Ala	
				320					325					330	
Arg	Leu	Ser	Trp	Thr	Gln	Arg	Gly	Gln	Val	Leu	Ser	Pro	Ser	Gln	
				335					340					345	
Pro	Ser	Asp	Pro	Gly	Val	Leu	Glu	Leu	Pro	Arg	Val	Gln	Val	Glu	
				350					355					360	
His	Glu	Gly	Glu	Phe	Thr	Cys	His	Ala	Arg	His	Pro	Leu	Gly	Ser	
				365					370					375	
Gln	His	Val	Ser	Leu	Ser	Leu	Ser	Val	His	Tyr	Lys	Lys	Gly	Leu	
				380					385					390	
Ile	Ser	Thr	Ala	Phe	Ser	Asn	Gly	Ala	Phe	Leu	Gly	Ile	Gly	Ile	
				395					400					405	
Thr	Ala	Leu	Leu	Phe	Leu	Cys	Leu	Ala	Leu	Ile	Ile	Met	Lys	Ile	
				410					415					420	
Leu	Pro	Lys	Arg	Arg	Thr	Gln	Thr	Glu	Thr	Pro	Arg	Pro	Arg	Phe	
				425					430					435	
Ser	Arg	His	Ser	Thr	Ile	Leu	Asp	Tyr	Ile	Asn	Val	Val	Pro	Thr	
				440					445					450	
Ala	Gly	Pro	Leu	Ala	Gln	Lys	Arg	Asn	Gln	Lys	Ala	Thr	Pro	Asn	
				455					460					465	
Ser	Pro	Arg	Thr	Pro	Pro	Pro	Pro	Gly	Ala	Pro	Ser	Pro	Glu	Ser	
				470					475					480	
Lys	Lys	Asn	Gln	Lys	Lys	Gln	Tyr	Gln	Leu	Pro	Ser	Phe	Pro	Glu	
				485					490					495	
Pro	Lys	Ser	Ser	Thr	Gln	Ala	Pro	Glu	Ser	Gln	Glu	Ser	Gln	Glu	
				500					505					510	
Glu	Leu	His	Tyr	Ala	Thr	Leu	Asn	Phe	Pro	Gly	Val	Arg	Pro	Arg	
				515					520					525	
Pro	Glu	Ala	Arg	Met	Pro	Lys	Gly	Thr	Gln	Ala	Asp	Tyr	Ala	Glu	
				530					535					540	
Val	Lys	Phe	Gln												

<210> 260
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 260
caaagcctgc gcctggtctg tg 22

<210> 261
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 261
ttctggagcc cagaggggtgc tgag 24

<210> 262
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 262
ggagctgcca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263
<211> 2857
<212> DNA
<213> Homo sapiens

<400> 263
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actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100
caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150
ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200
aatgaatacg actagtcac acatcggcca gctaagatct gatttagaca 250
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350
tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400
tcgctactgg aagggctgtg gaacctgagt ctgagtttgt catcaaagtt 450

tcggatatca atgacaatga accaaaaattc ctagatgaac cttatgaggc 500
cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550
caagtgatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600
agcttacttc aaggccagcc atatTTTTtct gttgaaccaa caacaggagt 650
cataagaata tcttctaaaa tggatagaga actgcaagat gagtattggg 700
taatcattca agccaaggac atgattggtc agccaggagc gttgtctgga 750
acaacaagtg tattaattaa actttcagat gttaatgaca ataagcctat 800
atttaaagaa agtttatacc gcttgactgt ctctgaatct gcacccactg 850
ggacttctat aggaacaatc atggcatatg ataatgacat aggagagaat 900
gcagaaatgg attacagcat tgaagaggat gattcgcaaa catttgacat 950
tattactaat catgaaactc aagaaggaat agttatatta aaaaagaaaag 1000
tggattttga gcaccagaac cactacggta ttagagcaaa agttaaaaaac 1050
catcatgttc ctgagcagct catgaagtac cacactgagg cttccaccac 1100
tttcattaag atccagggtg aagatgttga tgagcctcct cttttcctcc 1150
ttccatatta tgtatttgaa gtttttgaag aaaccccaca gggatcattt 1200
gtaggcgtgg tgtctgccac agaccagac aataggaaat ctctatcag 1250
gtattctatt actaggagca aagtgttcaa tatcaatgat aatggtacaa 1300
tcactacaag taactcactg gatcgtgaaa tcagtgcttg gtacaaccta 1350
agtattacag ccacagaaaa atacaatata gaacagatct cttcgatccc 1400
actgtatgtg caagttctta acatcaatga tcatgtcctt gagttctctc 1450
aatactatga gacttatgtt tgtgaaaatg caggctctgg tcaggtaatt 1500
cagactatca gtgcagtgga tagagatgaa tccatagaag agcaccattt 1550
ttactttaat ctatctgtag aagacactaa caattcaagt ttacaatca 1600
tagataatca agataacaca gctgtcattt tgactaatag aactggtttt 1650
aaccttcaag aagaacctgt cttctacatc tccatcttaa ttgccgacaa 1700
tggaatcccg tcacttacaa gtacaaacac ccttaccatc catgtctgtg 1750
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ctttccatgg gattcaagac agaagttatc attgctattc tcatttgcat 1850
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gaaaacagat tctatttcct gagaaaagtg aagatttcag agagaatata 1950
 ttccaatatg atgatgaagg ggggtggagaa gaagatacag aggcctttga 2000
 tatagcagag ctgaggagta gtaccataat gcgggaacgc aagactcgga 2050
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 ttattttaag ctacctacat gctgtcattg aacagagatg tggggagaaa 2550
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 aatgtaggaa gatattaaaa gtagatgaga ggacacaaga tgtagtcgat 2650
 ccttatgcga ttatatcatt atttacttag gaaagagtaa aaataccaaa 2700
 cgagaaaatt taaaggagca aaaatttgca agtcaaataa aaatgtacaa 2750
 atcgagataa catttacatt totatcatat tgacatgaaa attgaaaatg 2800
 tatagtcaga gaaattttca tgaattattc catgaagtat tgtttccttt 2850
 atttaaa 2857

<210> 264
 <211> 772
 <212> PRT
 <213> Homo sapiens

<400> 264
 Met Asn Cys Tyr Leu Leu Leu Arg Phe Met Leu Gly Ile Pro Leu
 1 5 10 15
 Leu Trp Pro Cys Leu Gly Ala Thr Glu Asn Ser Gln Thr Lys Lys
 20 25 30
 Val Lys Gln Pro Val Arg Ser His Leu Arg Val Lys Arg Gly Trp
 35 40 45
 Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser
 50 55 60

09078187-101501

His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn	
				65					70					75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	
				80					85					90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu	
				95					100					105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	
				110					115					120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val	
				125					130					135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	
				140					145					150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr	
				155					160					165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	
				170					175					180	
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro	
				185					190					195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser	
				200					205					210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln	
				215					220					225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr	
				230					235					240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile	
				245					250					255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro	
				260					265					270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile	
				275					280					285	
Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser	
				290					295					300	
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile	
				305					310					315	
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr	
				320					325					330	
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu	
				335					340					345	
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln	

350										355					360				
Val	Glu	Asp	Val	Asp	Glu	Pro	Pro	Leu	Phe	Leu	Leu	Pro	Tyr	Tyr					
				365					370					375					
Val	Phe	Glu	Val	Phe	Glu	Glu	Thr	Pro	Gln	Gly	Ser	Phe	Val	Gly					
				380					385					390					
Val	Val	Ser	Ala	Thr	Asp	Pro	Asp	Asn	Arg	Lys	Ser	Pro	Ile	Arg					
				395					400					405					
Tyr	Ser	Ile	Thr	Arg	Ser	Lys	Val	Phe	Asn	Ile	Asn	Asp	Asn	Gly					
				410					415					420					
Thr	Ile	Thr	Thr	Ser	Asn	Ser	Leu	Asp	Arg	Glu	Ile	Ser	Ala	Trp					
				425					430					435					
Tyr	Asn	Leu	Ser	Ile	Thr	Ala	Thr	Glu	Lys	Tyr	Asn	Ile	Glu	Gln					
				440					445					450					
Ile	Ser	Ser	Ile	Pro	Leu	Tyr	Val	Gln	Val	Leu	Asn	Ile	Asn	Asp					
				455					460					465					
His	Ala	Pro	Glu	Phe	Ser	Gln	Tyr	Tyr	Glu	Thr	Tyr	Val	Cys	Glu					
				470					475					480					
Asn	Ala	Gly	Ser	Gly	Gln	Val	Ile	Gln	Thr	Ile	Ser	Ala	Val	Asp					
				485					490					495					
Arg	Asp	Glu	Ser	Ile	Glu	Glu	His	His	Phe	Tyr	Phe	Asn	Leu	Ser					
				500					505					510					
Val	Glu	Asp	Thr	Asn	Asn	Ser	Ser	Phe	Thr	Ile	Ile	Asp	Asn	Gln					
				515					520					525					
Asp	Asn	Thr	Ala	Val	Ile	Leu	Thr	Asn	Arg	Thr	Gly	Phe	Asn	Leu					
				530					535					540					
Gln	Glu	Glu	Pro	Val	Phe	Tyr	Ile	Ser	Ile	Leu	Ile	Ala	Asp	Asn					
				545					550					555					
Gly	Ile	Pro	Ser	Leu	Thr	Ser	Thr	Asn	Thr	Leu	Thr	Ile	His	Val					
				560					565					570					
Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln					
				575					580					585					
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala					
				590					595					600					
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr					
				605					610					615					
Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys					
				620					625					630					
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly					
				635					640					645					

Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg
650 655 660

Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser
665 670 675

Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro
680 685 690

Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu
695 700 705

Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr
710 715 720

Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser
725 730 735

Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu
740 745 750

Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly
755 760 765

Ser Ala Val Gln Ser Asn Asn
770

<210> 265
<211> 349
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 24, 60, 141, 226, 228, 249, 252
<223> unknown base

<400> 265
atttcaaggc cagccatatt tttntgttga accaacaaca ggagtcataa 50
gaatatttttn taaaatggat agagaactgc aagatgagta ttgggtaatc 100
attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150
aagtgtatta attaaacttt cagatgttaa tgacaataag cctatatatta 200
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
aatggattac agcattgaag aggatgattc gcaaacatit gacattatt 349

<210> 266
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg caccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

gcaacctcag cttctagtat ccagactcca gcgcgcgccc gggcgcgagc 50

cccaaccccg acccagagct tctccagcgg cggcgcagcg agcagggctc 100

cccgccttaa cttcctccgc ggggcccagc caccttcggg agtccgggtt 150

gcccacctgc aaactctccg cttctgcac ctgccacccc tgagccagcg 200

cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250

cattctcgcc ttctgggat ggatcggcgc catcgtcagc actgccctgc 300

cccagtggag gatttactcc tatgccggcg acaacatcgt gaccgcccag 350

gccatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400

gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450

aagcaacccg tgccctgatg gtgggttgga tcctcctggg agtgatagca 500

atctttgtgg ccaccgttg catgaagtgt atgaagtgtc tggaagacga 550

tgaggtgcag aagatgagga tggctgtcat tgggggtgcg atatttcttc 600

ttgcaggctct ggctatittha gttgccacag catggtatgg caatagaatc 650
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 acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950
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 tgctagactt tctggagtga taatctggtg acaaatttc tctctgtagc 1950
 tgtaagcaag tcaacttaac tttctacctc tttttctat ctgccaaatt 2000
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acacgtacct tcatgtgatt cactgccttc ctctctctac cagtctatct 2200
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gatgttggtg ggatccagtg agatagaata catgtaagtg tgggtttgta 2650
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<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

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Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp
20 25 30

Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala
35 40 45

Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly
50 55 60

Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser
65 70 75

Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly Ile Leu Leu
80 85 90

Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met
95 100 105

Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val
110 115 120

Ile Gly Gly Ala	Ile Phe Leu Leu Ala	Gly Leu Ala Ile Leu Val
125		135
Ala Thr Ala Trp	Tyr Gly Asn Arg Ile	Val Gln Glu Phe Tyr Asp
140		150
Pro Met Thr Pro	Val Asn Ala Arg Tyr	Glu Phe Gly Gln Ala Leu
155		165
Phe Thr Gly Trp	Ala Ala Ala Ser Leu	Cys Leu Leu Gly Gly Ala
170		180
Leu Leu Cys Cys	Ser Cys Pro Arg Lys	Thr Thr Ser Tyr Pro Thr
185		195
Pro Arg Pro Tyr	Pro Lys Pro Ala Pro	Ser Ser Gly Lys Asp Tyr
200		210

Val

<210> 271
 <211> 564
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 21, 69, 163, 434, 436, 444
 <223> unknown base

<400> 271
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 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150
 ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250
 tgatgggtggg tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300
 gttggcatga agtgatatga gtgcttggaa gacgatgagg tgcagaagat 350
 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
 ttttagttgc cacagcatgg tatggcaata gaancnttca acanttttat 450
 gaccctatga cccagtgcaa tgccaggtac gaatttggtc aggctctctt 500
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550
 gctgttcctg tccc 564

<210> 272
 <211> 498

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341
<223> unknown base

<400> 272
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tccagctgtt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100
cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150
acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtccctgcgtg 200
tcgcagagca ccgggcagat ccagtgcaaa gtctttgact cccttgctga 250
atctgagcag cacattgcaa gcaacccgtg ccttgatggg ggttggcatc 300
ctcctgggag tgatagcaat cttnttggcc accgttgtnn ntgaagtgtg 350
tgaagtgtt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400
gggggcgcca tatttcttct tgcaggctctg gctatttttag ttgccacagc 450
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273
<211> 552
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273
gggcccgacc attatccaac cgggntcact gttggctcat ctccctcctg 50
gatgaancgc gccatcntca gactccctgc cccatggaga tttnnccat 100
gctggcgaca acatcntgac cccagccat gtacgagggg ctttgaacgt 150
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200
tgctgaatct gngcagcaca ttgcagcaac ccttgccctg atggtgggtg 250
gcacccctcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gcttgaaga cgatgagggt cagaagatga ggatggctgt 350
cattgggggc gcgatatttc ttcttgagc tctggctatt tnnngttgcc 400
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450

cccagtcaat gccaggtacg aatttgggtca ggctctcttc actggctggg 500
 ctgctgcttc tctctgcctt ctgggaggtg cctactttg ctgttcctgc 550
 ga 552

<210> 274
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407
 <223> unknown base

<400> 274
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 tggaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100
 ttaccgaggg gctttgatg tcntgcntgt cgcagagcac cgggcagatc 150
 ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200
 caaccctgctc cttgatgggg ttggcatcct cctgggagtg atagcaacct 250
 ttgtggccac cgttggcatg aagtgtatga agtgcttgga agacgatgag 300
 gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350
 caggtctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400
 cnnngnnntct atgaccctat gaccccagtc aatgccaggt acgaatttgg 450
 tcaggctctc ttcactggct gggctgctgc ttctctctgc cttctgggag 500
 gtgccctact ttgctgttcc tgtccc 526

<210> 275
 <211> 398
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274
 <223> unknown base

<400> 275
 agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50
 gcagcacatt ncaagcaacc ccttgccctg aaggtgggtg ncatcccccc 100
 tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150
 gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250
 tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300
 tgccaggtac gaatttggtc aggctctctt cactggctgg gctgctgctt 350
 ctctctgcct tctgggaggt gccctacttt gctgttcctg tccccgaa 398

<210> 276
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476
 <223> unknown base

<400> 276
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 gagcagcaca ttgcaagcaa cccgtgcctt gatggtggtt ggcactctcc 200
 tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250
 tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300
 cgcgatattt cttnttgca gtctggctat tttagttgcc acagcatggt 350
 atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400
 gccaggtacg aatttggtca ggctttnttc actggctggg ctgctgcttn 450
 tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277
 <211> 200
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 34, 87, 138, 147, 163, 165-166, 172
 <223> unknown base

<400> 277
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 gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278
 <211> 542
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 26, 43, 55, 77, 198, 361-362, 391-392, 396
 <223> unknown base

<400> 278
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 aagtctttga ctcttgctg aatctgagca gcacattgca agcaacctg 200
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 gctattttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400
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<210> 279
 <211> 548
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 90, 115, 147, 228, 387
 <223> unknown base

<400> 279
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 tgtcgcagag caccgggcag atccagtgc aagtctttga ctcttgctg 200
 aatctgagca gcacattgca agcaacctg ccttgatggt ggttggcatc 250
 ctctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300
 gaagtgttg gaagacgat aggtgcagaa gatgaggatg gctgtcattg 350

ggggcgcat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450
tcaatgccag gtacgaattt ggtcaggctc tcttcactgg ctgggctgct 500
gcttctctct gccttctggg aggtgcccta ctttgctggt cctgcgaa 548

<210> 280
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
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<210> 281
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 281
gtgtcacacg tagtctttcc cgctgg 26

<210> 282
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 282
ctgcagctgt tgggcttcat tctcgccctc ctgggatgga tcg 43

<210> 283
<211> 2285
<212> DNA
<213> Homo sapiens

<400> 283
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taaagcgggc gcagcattaa cgcttcccgc cccggtgacc tctcaggggt 200
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aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300
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catgtttct tattgtcaca agagtacagt taatgctgcg tgctgctgaa 1750

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tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000
actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050
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gcgagggcac cagcagttgt ggggtggggag caaggaaga gagaaactct 2150
tcagcgaatc cttctagtag tagttgagag tttgactgtg aattaatttt 2200
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agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met	Ala	Lys	Val	Glu	Gln	Val	Leu	Ser	Leu	Glu	Pro	Gln	His	Glu
1				5					10					15
Leu	Lys	Phe	Arg	Gly	Pro	Phe	Thr	Asp	Val	Val	Thr	Thr	Asn	Leu
				20					25					30
Lys	Leu	Gly	Asn	Pro	Thr	Asp	Arg	Asn	Val	Cys	Phe	Lys	Val	Lys
				35					40					45
Thr	Thr	Ala	Pro	Arg	Arg	Tyr	Cys	Val	Arg	Pro	Asn	Ser	Gly	Ile
				50					55					60
Ile	Asp	Ala	Gly	Ala	Ser	Ile	Asn	Val	Ser	Val	Met	Leu	Gln	Pro
				65					70					75
Phe	Asp	Tyr	Asp	Pro	Asn	Glu	Lys	Ser	Lys	His	Lys	Phe	Met	Val
				80					85					90
Gln	Ser	Met	Phe	Ala	Pro	Thr	Asp	Thr	Ser	Asp	Met	Glu	Ala	Val
				95					100					105
Trp	Lys	Glu	Ala	Lys	Pro	Glu	Asp	Leu	Met	Asp	Ser	Lys	Leu	Arg
				110					115					120
Cys	Val	Phe	Glu	Leu	Pro	Ala	Glu	Asn	Asp	Lys	Pro	His	Asp	Val
				125					130					135
Glu	Ile	Asn	Lys	Ile	Ile	Ser	Thr	Thr	Ala	Ser	Lys	Thr	Glu	Thr
				140					145					150

Pro	Ile	Val	Ser	Lys	Ser	Leu	Ser	Ser	Ser	Leu	Asp	Asp	Thr	Glu
				155					160					165
Val	Lys	Lys	Val	Met	Glu	Glu	Cys	Lys	Arg	Leu	Gln	Gly	Glu	Val
				170					175					180
Gln	Arg	Leu	Arg	Glu	Glu	Asn	Lys	Gln	Phe	Lys	Glu	Glu	Asp	Gly
				185					190					195
Leu	Arg	Met	Arg	Lys	Thr	Val	Gln	Ser	Asn	Ser	Pro	Ile	Ser	Ala
				200					205					210
Leu	Ala	Pro	Thr	Gly	Lys	Glu	Glu	Gly	Leu	Ser	Thr	Arg	Leu	Leu
				215					220					225
Ala	Leu	Val	Val	Leu	Phe	Phe	Ile	Val	Gly	Val	Ile	Ile	Gly	Lys
				230					235					240

Ile Ala Leu

<210> 285
 <211> 418
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 40, 53, 68, 119, 134, 177-178, 255
 <223> unknown base

<400> 285
 gtcagtcttc tagattgtcc ttatcccacc tttcaaccan tactcacatt 50
 tcnagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100
 ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150
 cagcagtttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200
 cttctagtac tagttgagag tttgactgtg aattaatttt atgccataaa 250
 agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
 taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
 ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
 gttaacttta aaatgagc 418

<210> 286
 <211> 543
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 73, 97

<223> unknown base

<400> 286

tattgtaaag gccattttaa accattggta ggccttggta catgatgctg 50
gattacctcc ttaaatgaca ccttcctcg cctgttgggtg ctggccnttg 100
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250
aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgagagg 300
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350
gttcacttaa agggaccaag cttaaattgta ttggttcatg tagtgaagtc 400
aaactgttat tcagagatgt ttaatgcata ttttaacttat ttaatgtatt 450
tcattctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242

<223> unknown base

<400> 287

ccctgggtgg tttgttcttt aattcgttgg tgtaattntt gggaagattg 50
ctttagtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100
catatccatg ggattttaaatt ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaaat gtatagtaac 270

<210> 288

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base

<400> 288
 ggtggcccat tcccggccca ggctgctttc cggtnntcag ttctgtccaa 50
 gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
 gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
 actgattgac ccagcgcttt ggaaataaat ggcagtgcct tgttcantta 200
 aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250
 attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300
 tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
 ntgttgggtg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400
 ttggagagtc tggatcatgtg gaggtggg 428

<210> 289
 <211> 320
 <212> DNA
 <213> Homo sapiens

<400> 289
 tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50
 atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100
 tactcgtcat aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150
 gaaataaatg gcagtgcctt gtacacttaa agggaccaag ctaaatttgt 200
 attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
 atttaactta tttaatgtat ttcattctcat gttttcttat tgtcacaaga 300
 gtacagttaa tgctgcgtgc 320

<210> 290
 <211> 609
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
 447, 481, 513, 532, 584, 598
 <223> unknown base

<400> 290
 aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50
 gaaacntgn gtaatgccac aatggcatat tgtaaattgc attttaaaca 100
 ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150
 cttcctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200

ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250
cccaggctgc tttccgtgtc ttcagttctg tccaagccat cagctccttg 300
ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
cagangtant ngtcataagt gagaggcgtg tgttgantga ttgacccagc 400
gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450
atttgatttg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500
atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550
acaagggtag agttaatgct gcgtgctgct gaantctggt gggagaantg 600
gtattgctg 609

<210> 291
<211> 493
<212> DNA
<213> Homo sapiens

<400> 291
ggcccttggg gagctggagc ccagcatgct ggggagtgcg gtcagctcca 50
cacagtagtc cccacgtggc ccaactcccgg cccaggctgc tttccgtgtc 100
ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150
aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
gagaggcgtg tgttgactga ttgacccagc gctttggaaa taaatggcag 250
tgctttgttc acttaaaggg accaagctaa atttgatttg gttcatgtag 300
tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350
atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400
gcgtgctgct gaactctggt gggagaactg gtattgctgc tggagggctg 450
tgggctcctc tgtctctgga gagtctgggc atgtggaggt ggg 493

<210> 292
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 292
gcaccaccgt aggtacttgt gtgaggc 27

<210> 293
<211> 23
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcgggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50

ggctggctga gaggctccca gctgcagcgt ccccgccgc ctctcgga 100

gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150

gtctcacttt gttgcccagg ctggagttca gtgccatgat catggtttac 200

tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250

acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300

atttttcacc cctgggtgga cctcattga tggatctgaa atggaatggg 350

attttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400

ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450

tacagtgtgt ggcacgaat gccagaaaga actcccaact ccagccttt 500

ctgaattgga ggattatctt tctatgaga ctgtctttga gaatggcacc 550

cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600

aaatatcacc acaaaggag tatctgttag gagaaagaga cagggtgatg 650

gcaccgacag caggttcagc atcttgga aaaggttctt aaccaatttc 700

cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750

ttcccctcag catgtttctaa ctgtgcccc ctgtgttcat gatggaaagg 800

actatgtcaa agggagtaaa aagctaagg tagggttgtt gaagatgagg 850

aataaaagtg gaggcaagaa acgtcgaggt tctaagagga gcaggagaga 900
agctagtggg ggtgaccaa gagaggggtac cagagagcat ctgcaggaga 950
gagcgaaggg tgggagaaga agaaaaaat ctggccgggg tcagaggatt 1000
gccgaagggg ggccttcctt tcagtggacc cgggtcaaga atacccacat 1050
tccgaagggc tgggcaagag gaggcattgg ggacgctacc ttggactatg 1100
actatgctct tctggagctg aagcgtgctc acaaaaagaa atacatggaa 1150
cttggaatca gcccaacgat caagaaaatg cctgggtgaa tgatccactt 1200
ctcaggattt gataacgata gggctgatca gttgggtctat cggttttgca 1250
gtgtgtccga cgaatccaat gatctccttt accaatactg cgatgctgag 1300
tcgggctcca ccggttcggg ggtctatctg cgtctgaaag atccagacaa 1350
aaagaattgg aagcgcaaaa tcattgcggg ctactcaggg caccagtggg 1400
tgatgtcca cgggggttcag aaggactaca acgttgctgt tcgcatcact 1450
cccctaaaat acgccagat ttgcctctgg attcacggga acgatgcaa 1500
ttgtgcttac ggctaacaga gacctgaaac agggcgggtg atcatctaaa 1550
tcacagagaa aaccagctct gcttaccgta gtgagatcac ttcatagggt 1600
atgcctggac ttgaactctg tcaatagcat ttcaacattt ttcaaatca 1650
ggagattttc gtccatttaa aaaatgtata ggtgcagata ttgaaactag 1700
gtgggcactt caatgccaa tatatactct tctttacatg gtgatgagtt 1750
tcatttgtag aaaaattttg ttgccttctt aaaaattaga cacactttaa 1800
accttcaaac aggtattata aataacatgt gactccttaa tggacttatt 1850
ctcagggtcc tactctaaga agaatctaata aggatgctgg ttgtgtatta 1900
aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950
atagagacag aaagttacaa cacagtttgt actactctga gatggatcca 2000
ttcagctcat gccctcaatg tttatattgt gttatctggt gggctctggga 2050
catttagttt agtttttttg aagaattaca aatcagaaga aaaagcaagc 2100
attataaaca aaactaataa ctgttttact gctttaagaa ataacaatta 2150
caatgtgtat ttttaaaaaa tgggagaaat agtttgttct atgaaataaa 2200
cctagtttag aaatagggaa gctgagacat ttttaagatct caagttttta 2250
tttaactaat actcaaaata tggacttttc atgtatgcat agggaagaca 2300

cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350
 atacattcta tgtatgaggt gctacatttt taggacaaaag aattctgtaa 2400
 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450
 tgaggactat aggggtgaatt ctctgattag taattttaga tatgtccttt 2500
 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296
 <211> 413
 <212> PRT
 <213> Homo sapiens

<400> 296
 Met Glu Asn Met Leu Leu Trp Leu Ile Phe Phe Thr Pro Gly Trp
 1 5 10 15
 Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His
 20 25 30
 Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu
 35 40 45
 Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr
 50 55 60
 Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu
 65 70 75
 Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn
 80 85 90
 Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu
 95 100 105
 Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg
 110 115 120
 Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp
 125 130 135
 Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu
 140 145 150
 Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu
 155 160 165
 Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly
 170 175 180
 Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser
 185 190 195
 Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala
 200 205 210

Ser Gly Gly Asp	Gln Arg Glu Gly Thr	Arg Glu His Leu Gln Glu
215	220	225
Arg Ala Lys Gly	Gly Arg Arg Arg Lys	Lys Ser Gly Arg Gly Gln
230	235	240
Arg Ile Ala Glu	Gly Arg Pro Ser Phe	Gln Trp Thr Arg Val Lys
245	250	255
Asn Thr His Ile	Pro Lys Gly Trp Ala	Arg Gly Gly Met Gly Asp
260	265	270
Ala Thr Leu Asp	Tyr Asp Tyr Ala Leu	Leu Glu Leu Lys Arg Ala
275	280	285
His Lys Lys Lys	Tyr Met Glu Leu Gly	Ile Ser Pro Thr Ile Lys
290	295	300
Lys Met Pro Gly	Gly Met Ile His Phe	Ser Gly Phe Asp Asn Asp
305	310	315
Arg Ala Asp Gln	Leu Val Tyr Arg Phe	Cys Ser Val Ser Asp Glu
320	325	330
Ser Asn Asp Leu	Leu Tyr Gln Tyr Cys	Asp Ala Glu Ser Gly Ser
335	340	345
Thr Gly Ser Gly	Val Tyr Leu Arg Leu	Lys Asp Pro Asp Lys Lys
350	355	360
Asn Trp Lys Arg	Lys Ile Ile Ala Val	Tyr Ser Gly His Gln Trp
365	370	375
Val Asp Val His	Gly Val Gln Lys Asp	Tyr Asn Val Ala Val Arg
380	385	390
Ile Thr Pro Leu	Lys Tyr Ala Gln Ile	Cys Leu Trp Ile His Gly
395	400	405
Asn Asp Ala Asn	Cys Ala Tyr Gly	
410		

<210> 297
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 297
 gcatctgcag gagagagcga aggg 24

<210> 298
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 298
catcgttccc gtgaatccag aggc 24

<210> 299
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 299
gaaggaggc cttcctttca gtggacccgg gtcaagaata cccac 45

<210> 300
<211> 1869
<212> DNA
<213> Homo sapiens

<400> 300
aatgtgagag gggctgatgg aagctgatag gcaggactgg agtgtttagca 50
ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150
gcaactcctg gcacactgct cctctttctg gctttcctgc tcctgagttc 200
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250
gcccattggag tgaatgctca cgcacctgcg ggggaggggc ctccactct 300
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350
cagaacatgc agtaatgtgg actgcccacc agaagcaggt gatttccgag 400
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagttttat 450
gaatggcttc ctgtgtctaa tgaccctgac aacccatgtt cactcaagtg 500
ccaagccaaa ggaacaaccc tggttgttga actagcacct aaggctcttag 550
atggtacgcg ttgctataca gaatcttttg atatgtgcat cagtggttta 600
tgccaaattg ttggtgcga tcaccagctg ggaagcaccg tcaaggaaga 650
taactgtggg gtctgcaacg gagatgggtc cacctgccgg ctggtccgag 700
ggcagtataa atcccagctc tccgcaacca aatcggatga tactgtgggtt 750
gcacttcctt atggaagtag acatattcgc cttgtcttaa aaggctcctga 800
tcacttatat ctggaaacca aaaccctcca ggggactaaa ggtgaaaaca 850
gtctcagctc cacaggaact ttccttgtgg acaattctag tgtggacttc 900

cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc 950
agatttcatt gtcaagattc gtaactcggg ctccgctgac agtacagtcc 1000
agttcatctt ctatcaaccc atcatccacc gatggaggga gacggatttc 1050
tttccttgct cagcaacctg tggaggagggt tatcagctga catcggctga 1100
gtgctacgat ctgaggagca accgtgtggt tgctgaccaa tactgtcact 1150
attaccacaga gaacatcaaa cccaaaccca agcttcagga gtgcaacttg 1200
gatccttgtc cagccagtga cggatacaag cagatcatgc cttatgacct 1250
ctaccatccc cttcctcggg gggaggccac cccatggacc gcgtgctcct 1300
cctcgtgtgg ggggggcatc cagagccggg cagtttcctg tgtggaggag 1350
gacatccagg ggcattgtac ttcagtggaa gagtggaaat gcatgtacac 1400
ccctaagatg cccatcgcgc agccctgcaa catttttgac tgccctaaat 1450
ggctggcaca ggagtgggtc ccgtgcacag tgacatgtgg ccagggcctc 1500
agataccgtg tggctcctctg catcgaccat cgaggaatgc acacaggagg 1550
ctgtagccca aaaacaaagc cccacataaa agaggaatgc atcgtaccca 1600
ctccctgcta taaacccaaa gagaaacttc cagtcgaggc caagttgcca 1650
tggttcaaac aagctcaaga gctagaagaa ggagctgctg tgtcagagga 1700
gccctcgtaa gttgtaaaag cacagactgt tctatatttg aaactgtttt 1750
gtttaaagaa agcagtgtct cactggttgt agctttcatg ggttctgaac 1800
taagtgtaat catctacca aagctttttg gctctcaaat taaagattga 1850
ttagtttcaa aaaaaaaaaa 1869

<210> 301
<211> 525
<212> PRT
<213> Homo sapiens

<400> 301
Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe
1 5 10 15
Leu Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu
20 25 30
Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys
35 40 45
Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys
50 55 60

Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr			
				65					70					75			
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala			
				80					85					90			
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe			
				95					100					105			
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser			
				110					115					120			
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala			
				125					130					135			
Pro	Lys	Val	Leu	Asp	Gly	Thr	Arg	Cys	Tyr	Thr	Glu	Ser	Leu	Asp			
				140					145					150			
Met	Cys	Ile	Ser	Gly	Leu	Cys	Gln	Ile	Val	Gly	Cys	Asp	His	Gln			
				155					160					165			
Leu	Gly	Ser	Thr	Val	Lys	Glu	Asp	Asn	Cys	Gly	Val	Cys	Asn	Gly			
				170					175					180			
Asp	Gly	Ser	Thr	Cys	Arg	Leu	Val	Arg	Gly	Gln	Tyr	Lys	Ser	Gln			
				185					190					195			
Leu	Ser	Ala	Thr	Lys	Ser	Asp	Asp	Thr	Val	Val	Ala	Leu	Pro	Tyr			
				200					205					210			
Gly	Ser	Arg	His	Ile	Arg	Leu	Val	Leu	Lys	Gly	Pro	Asp	His	Leu			
				215					220					225			
Tyr	Leu	Glu	Thr	Lys	Thr	Leu	Gln	Gly	Thr	Lys	Gly	Glu	Asn	Ser			
				230					235					240			
Leu	Ser	Ser	Thr	Gly	Thr	Phe	Leu	Val	Asp	Asn	Ser	Ser	Val	Asp			
				245					250					255			
Phe	Gln	Lys	Phe	Pro	Asp	Lys	Glu	Ile	Leu	Arg	Met	Ala	Gly	Pro			
				260					265					270			
Leu	Thr	Ala	Asp	Phe	Ile	Val	Lys	Ile	Arg	Asn	Ser	Gly	Ser	Ala			
				275					280					285			
Asp	Ser	Thr	Val	Gln	Phe	Ile	Phe	Tyr	Gln	Pro	Ile	Ile	His	Arg			
				290					295					300			
Trp	Arg	Glu	Thr	Asp	Phe	Phe	Pro	Cys	Ser	Ala	Thr	Cys	Gly	Gly			
				305					310					315			
Gly	Tyr	Gln	Leu	Thr	Ser	Ala	Glu	Cys	Tyr	Asp	Leu	Arg	Ser	Asn			
				320					325					330			
Arg	Val	Val	Ala	Asp	Gln	Tyr	Cys	His	Tyr	Tyr	Pro	Glu	Asn	Ile			
				335					340					345			
Lys	Pro	Lys	Pro	Lys	Leu	Gln	Glu	Cys	Asn	Leu	Asp	Pro	Cys	Pro			

350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met	Pro Tyr Asp Leu Tyr His	
365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro	Trp Thr Ala Cys Ser Ser	
380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg	Ala Val Ser Cys Val Glu	
395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser	Val Glu Glu Trp Lys Cys	
410	415	420
Met Tyr Thr Pro Lys Met Pro Ile Ala	Gln Pro Cys Asn Ile Phe	
425	430	435
Asp Cys Pro Lys Trp Leu Ala Gln Glu	Trp Ser Pro Cys Thr Val	
440	445	450
Thr Cys Gly Gln Gly Leu Arg Tyr Arg	Val Val Leu Cys Ile Asp	
455	460	465
His Arg Gly Met His Thr Gly Gly Cys	Ser Pro Lys Thr Lys Pro	
470	475	480
His Ile Lys Glu Glu Cys Ile Val Pro	Thr Pro Cys Tyr Lys Pro	
485	490	495
Lys Glu Lys Leu Pro Val Glu Ala Lys	Leu Pro Trp Phe Lys Gln	
500	505	510
Ala Gln Glu Leu Glu Glu Gly Ala Ala	Val Ser Glu Glu Pro Ser	
515	520	525

<210> 302
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<400> 302
 cggacgcgtg ggcggcggct gcggaactcc cgtggagggg ccggtgggcc 50
 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100
 ctgggcgggg cgctgtggct ggcggcccg cggttcgtgg ggcccagggt 150
 ccagcggctg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgcccag 250
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300
 cgccgaggag gcggcgggtc agctccggcg cgagctccgc caggccgcgg 350
 agtgcgggcc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400
 gagctggacc tcgcctcgct gcgctcgggt gcgccttct gccaggaaat 450

gctccaggaa gagcctagggc tggatgtctt gatcaataac gcagggatct 500
tccagtgtccc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550
gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600
caaaagttca gctcccagca ggattgtggt agtttcttcc aaactttata 650
aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700
aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750
ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgttgc 800
atcctgggtat tgtacggaca aatctgggga ggacataca cattccactg 850
ttgggtcaaac cactcttcaa tttgggtgtca tgggcttttt tcaaaaactcc 900
agtagaagggt gcccagactt ccattttattt ggctcttca cctgaggtag 950
aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000
cccaaagcta tggatgaatc tggtgcaaga aaactctggg atatcagtga 1050
agtgtgggtt ggctgtctaa aataggaaca aggagtataa gagctgttta 1100
taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150
acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200
ggtacatgtg ggtattttgg agttactgaa aaattatttt tgggataaga 1250
gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300
aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
tggatgacat attaataattt gtcagaatta agtgactcaa agtgctatcg 1400
agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
ttactacaat gtttggtggt tgtgtggaaa ttatctgcct ggtgtgtgca 1500
cacaagtctt acttggaata aatttactgg tac 1533

<210> 303
<211> 336
<212> PRT
<213> Homo sapiens

<400> 303
Met Ala Val Ala Thr Ala Ala Ala Val Leu Ala Ala Leu Gly Gly
1 5 10 15
Ala Leu Trp Leu Ala Ala Arg Arg Phe Val Gly Pro Arg Val Gln
20 25 30
Arg Leu Arg Arg Gly Gly Asp Pro Gly Leu Met His Gly Lys Thr
35 40 45

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala	
				50					55					60	
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg	
				65					70					75	
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu	
				80					85					90	
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly	
				95					100					105	
Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg	
				110					115					120	
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg	
				125					130					135	
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr	
				140					145					150	
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	
				155					160					165	
Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys	
				170					175					180	
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr	
				185					190					195	
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser	
				200					205					210	
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile	
				215					220					225	
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Gly	Thr	Asn	Val	
				230					235					240	
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly	
				245					250					255	
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu	
				260					265					270	
Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr	
				275					280					285	
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly	
				290					295					300	
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala	
				305					310					315	
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val	
				320					325					330	
Met	Val	Gly	Leu	Leu	Lys										

<210> 304
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 34, 62, 87, 221, 229
 <223> unknown base

<400> 304
 ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50
 gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100
 ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150
 gtgatcagga atgggtgtga ttgagaactt gttacttgaa gaaaaagaat 200
 tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250
 actgaaaaat tatttttggg ataagagaat ttcagcaaag atgttttaaa 300
 tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
 attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
 gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
 tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
 tggaaattat ctgcctggct t 521

<210> 305
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 305
 ccaggaaatg ctccaggaag agcc 24

<210> 306
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 306
 gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307
aacgcaggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308
<211> 1523
<212> DNA
<213> Homo sapiens

<400> 308
gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50
cggagcccag ccttttcta acccaacca acctagcca gtcccagccg 100
ccagcgctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150
cttctatcc ttaccgacc tcagatgctc cttctgctc ctggtaactt 200
gggtttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250
atagatgaaa ttttaaaca tgctgatgtt gctttagtaa atttttatgc 300
tgactggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350
ccgatgtcat taaggaagaa ttccaaatg aaaatcaagt agtgtttgcc 400
agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 450
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550
caaaaaagtg acccattca agaaattcgg gacttagcag aaatcaccac 600
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650
cggacaacta tagagttttt gaacgagtag cgaatatattt gcatgatgac 700
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850
gataaatgtg ttcctcttgt ccgagaaata acatttgaaa atggagagga 900
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000
agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050

acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100
ctattgacag ctttaggcatt atgtatgtgt ttggagactt caaagatgta 1150
ttaattcctg gaaaactcaa gcaattcgta ttgacttac attctggaaa 1200
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250
gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300
aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350
gctttaaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400
cctacgtggg ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450
tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309
<211> 406
<212> PRT
<213> Homo sapiens

<400> 309
Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser
1 5 10 15
Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu
20 25 30
Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn
35 40 45
Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe
50 55 60
Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile
65 70 75
Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val
80 85 90
Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser
95 100 105
Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys
110 115 120
Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr
125 130 135
Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu
140 145 150
Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly
155 160 165

Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg
				170					175					180
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe
				185					190					195
Gly	Asp	Val	Ser	Lys	Pro	Glu	Arg	Tyr	Ser	Gly	Asp	Asn	Ile	Ile
				200					205					210
Tyr	Lys	Pro	Pro	Gly	His	Ser	Ala	Pro	Asp	Met	Val	Tyr	Leu	Gly
				215					220					225
Ala	Met	Thr	Asn	Phe	Asp	Val	Thr	Tyr	Asn	Trp	Ile	Gln	Asp	Lys
				230					235					240
Cys	Val	Pro	Leu	Val	Arg	Glu	Ile	Thr	Phe	Glu	Asn	Gly	Glu	Glu
				245					250					255
Leu	Thr	Glu	Glu	Gly	Leu	Pro	Phe	Leu	Ile	Leu	Phe	His	Met	Lys
				260					265					270
Glu	Asp	Thr	Glu	Ser	Leu	Glu	Ile	Phe	Gln	Asn	Glu	Val	Ala	Arg
				275					280					285
Gln	Leu	Ile	Ser	Glu	Lys	Gly	Thr	Ile	Asn	Phe	Leu	His	Ala	Asp
				290					295					300
Cys	Asp	Lys	Phe	Arg	His	Pro	Leu	Leu	His	Ile	Gln	Lys	Thr	Pro
				305					310					315
Ala	Asp	Cys	Pro	Val	Ile	Ala	Ile	Asp	Ser	Phe	Arg	His	Met	Tyr
				320					325					330
Val	Phe	Gly	Asp	Phe	Lys	Asp	Val	Leu	Ile	Pro	Gly	Lys	Leu	Lys
				335					340					345
Gln	Phe	Val	Phe	Asp	Leu	His	Ser	Gly	Lys	Leu	His	Arg	Glu	Phe
				350					355					360
His	His	Gly	Pro	Asp	Pro	Thr	Asp	Thr	Ala	Pro	Gly	Glu	Gln	Ala
				365					370					375
Gln	Asp	Val	Ala	Ser	Ser	Pro	Pro	Glu	Ser	Ser	Phe	Gln	Lys	Leu
				380					385					390
Ala	Pro	Ser	Glu	Tyr	Arg	Tyr	Thr	Leu	Leu	Arg	Asp	Arg	Asp	Glu
				395					400					405

Leu

<210> 310
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure

<222> 36, 48
<223> unknown base

<400> 310
attaaggaag aatttcctaaa tgaaaatcaa gtagtntttg ccagagtnga 50
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
caaccctcaa attgttttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396
<223> unknown base

<400> 311
agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50
gagaggacna ggtgccgtg cctggagaat cctccgctgc cgtcggctcc 100
cggagcccag ccctttccta acccaaccca acctagcccn gtcccagccg 150
ccagcgcctg tcctgtcnc gganccagc gtnaccatgc atcctgccgt 200
cttcctatcc ttaccgacc tcagatgctc cttctgctc ctggttaactt 250
gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300
atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350
tgactgggtg cgtttcagtc agatgtggca tccaattttt gaggangctt 400
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
tgagaggcct ctctggaagt tg 22

<210> 313
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 313
 gtcagcgatc agtgaaagc 19

 <210> 314
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 314
 ccagaatgaa gtagctcggc 20

 <210> 315
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 315
 ccgactcaaaa atgcattgtc 20

 <210> 316
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 316
 catttggcag gaattgtcc 19

 <210> 317
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 317
 ggtgctatag gccaaagg 18

 <210> 318
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgtcttccta tccttaccgc acctcagatg ctcccttctg ctctg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50

cgctgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

tacctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tttttgtgca gcagagtggc ttacactggg totcaatatg 250

cccctcttgg catatcatat ttggagggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaacat catgaatgca gatattctag 350

catattgtca gaaggaagga tgggtgcaaat tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggc ccagttaagt gcatgcaaaa agccaccaaa 500

tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaa at gtttccacat 600
 ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650
 taaatggtat tacgtataaa ttaatataaa atgattacct ctggtgttga 700
 caggtttgaa ctgactctt ttaaggaaca gccataatcc tctgaatgat 750
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800
 cttgtagggc tcatttttgg ttcattgaaa cagtatctaa ttataaatta 850
 gctgtagata tcagggtgctt ctgatgaagt gaaaatgtat atctgactag 900
 tgggaaactt catgggtttc ctcatctgtc atgtcgatga ttatatatgg 950
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050
 taaatatact tgctttaatt cttaagcata agtaaactg atataaaaaat 1100
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaagtgtg 1150
 ttttatttgt aagacattac ttattaagaa attgggttatt atgcttactg 1200
 ttctaactctg gtggtaaaagg tattcttaag aatttgcagg tactacagat 1250
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu
 1 5 10 15
 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala
 20 25 30
 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys
 35 40 45
 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala
 50 55 60
 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu
 65 70 75
 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met
 80 85 90
 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr
 95 100 105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
 110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
 125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser
 140

<210> 323
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 323
 attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50
 tgtaataccc tgaatcccct tgtactccca gagtacctca tccacgcttt 100
 cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150
 atatgcccct cttggcatat catatttggg ggtatatgag tagaccagt 200
 atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250
 tctagcatat tgtcagaagg aaggatggtg caaattagct ttttatcttc 300
 tagcattttt ttactacctata tatggcatga tctatgtttt ggtgagctct 350
 tagaacaaca cacagaagaa ttggtccagt taagtgcattg caaaaagcca 400
 ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
 gaatctgata agttacttta aaaaatg 477

<210> 324
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 324
 tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 325
 caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tgggtgcaa tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100
ggacccaact ggggctcccc ccgctgctgc tgctgaccat ggccttggcc 150
ggaggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250
accctaagga agaggagtgtg tacgcatgtc agagagggttg caggctgttt 300
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400
atgcttgcca tcttgggtgc cagaatcagc tgccattcgc tgaactgaga 450
caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500

aactctggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550
tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600
gttatattcc agtctaagcc agaaatccag tacgcaccac atttggagca 650
ggagcctaca aatttgagag aatcatctct aagcaaaatg tcctatctgc 700
aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaaagt 750
gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800
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ttgctacagc tgtggagcag tatgttccct ctgagaagct gagtatctat 900
ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950
ttctcttggtg gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000
ctctacctac aaaagtgaat ctgtctcatt ctgaaattta agcatttttc 1050
ttttaaaaga caagtgtaat agacatctaa aattccactc ctcatagagc 1100
ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150
caaataaagt tactcaaatc tgtg 1174

<210> 330
<211> 323
<212> PRT
<213> Homo sapiens

<400> 330
Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly
1 5 10 15
Leu Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser
20 25 30
Gly Thr Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr
35 40 45
Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr
50 55 60
Tyr Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg
65 70 75
Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn
80 85 90
Arg Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser
95 100 105
Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln
110 115 120

Leu	Pro	Phe	Ala	Glu	Leu	Arg	Gln	Glu	Gln	Leu	Met	Ser	Leu	Met	
				125					130					135	
Pro	Lys	Met	His	Leu	Leu	Phe	Pro	Leu	Thr	Leu	Val	Arg	Ser	Phe	
				140					145					150	
Trp	Ser	Asp	Met	Met	Asp	Ser	Ala	Gln	Ser	Phe	Ile	Thr	Ser	Ser	
				155					160					165	
Trp	Thr	Phe	Tyr	Leu	Gln	Ala	Asp	Asp	Gly	Lys	Ile	Val	Ile	Phe	
				170					175					180	
Gln	Ser	Lys	Pro	Glu	Ile	Gln	Tyr	Ala	Pro	His	Leu	Glu	Gln	Glu	
				185					190					195	
Pro	Thr	Asn	Leu	Arg	Glu	Ser	Ser	Leu	Ser	Lys	Met	Ser	Tyr	Leu	
				200					205					210	
Gln	Met	Arg	Asn	Ser	Gln	Ala	His	Arg	Asn	Phe	Leu	Glu	Asp	Gly	
				215					220					225	
Glu	Ser	Asp	Gly	Phe	Leu	Arg	Cys	Leu	Ser	Leu	Asn	Ser	Gly	Trp	
				230					235					240	
Ile	Leu	Thr	Thr	Thr	Leu	Val	Leu	Ser	Val	Met	Val	Leu	Leu	Trp	
				245					250					255	
Ile	Cys	Cys	Ala	Thr	Val	Ala	Thr	Ala	Val	Glu	Gln	Tyr	Val	Pro	
				260					265					270	
Ser	Glu	Lys	Leu	Ser	Ile	Tyr	Gly	Asp	Leu	Glu	Phe	Met	Asn	Glu	
				275					280					285	
Gln	Lys	Leu	Asn	Arg	Tyr	Pro	Ala	Ser	Ser	Leu	Val	Val	Val	Arg	
				290					295					300	
Ser	Lys	Thr	Glu	Asp	His	Glu	Glu	Ala	Gly	Pro	Leu	Pro	Thr	Lys	
				305					310					315	
Val	Asn	Leu	Ala	His	Ser	Glu	Ile								
				320											

<210> 331
 <211> 350
 <212> DNA
 <213> Homo sapiens

<400> 331
 ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctaccctt 50
 gcacacctac cctaaggaag aggagttgta cgcattgtcag agagggttgca 100
 ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaactga 150
 actaaattgg aatgtgaatc tgcatgtaca gaagcatatt cccaatctga 200
 tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250

aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300
 tttcctctaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332
 <211> 562
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 47
 <223> unknown base

<400> 332
 cacactggcc ggatctttta gagtcctttg accttgacca agggtcngga 50
 aaacagcaac aagctgagct gctgtgacag agggaacaag atggcggcgc 100
 cgaagggagc ctttggggtga ggacccaact ggggctcccg ccgctgctgc 150
 tgctgaccat ggcccttgcc ggaggttcgg ggaccgcttc ggctgaagca 200
 ttgactcgg tcttggggtga tacggcgtct tgccaccggg cctgtcagtt 250
 gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300
 agagaggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350
 gacttaaadc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400
 ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450
 tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500
 atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550
 gatggactcc gc 562

<210> 333
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 333
 acaagctgag ctgctgtgac ag 22

<210> 334
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 335
atggccttgg ccggaggttc ggggaccgct tcggctgaag 40

<210> 336
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 336
gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50
cggcccggag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100
agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150
gcgacaagct gccggagctg caatggggccg cggtctggga ttcttgtttg 200
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250
cccccgaga cagcggcaca gaggtgcttc tgccaggta gtggttactt 300
ggatgattgt acctgtgatg ttgaaaccat tgatagattt aataactaca 350
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600
tctgagttag gaaacacaga aggtgttct tcagtggacc aagcatgatg 650
attcttcaga taacttctgt gaagctgatg acattcagtc cctgaagct 700
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750
accagatgct tgaaaaatat ggaatgtcat ctacgaagaa aactgtttta 800
agccacagac aattaaaga ctttaaatac ctttggtctt tggtcaaggg 850
acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900
aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950

tgcatttgag tgcaagatat cttttacaag agacctgggt agaaaagaaa 1000
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatttt ctctacttaa 1100
 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatgtt 1200
 acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350
 ttgttttaaa tgtcgtctgt ggggaaaagct tcagactcag ggtttgggca 1400
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550
 tcaggaaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650
 atagcaatga cagtcttaag ccaaacattt tatataaagt tgcttttgta 1700
 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800
 acaaatttta aagttaata ttgaataaaa ggaggattat caaattaaaa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337

<211> 468

<212> PRT

<213> Homo sapiens

<400> 337

Met	Gly	Arg	Gly	Trp	Gly	Phe	Leu	Phe	Gly	Leu	Leu	Gly	Ala	Val
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Trp	Leu	Leu	Ser	Ser	Gly	His	Gly	Glu	Glu	Gln	Pro	Pro	Glu	Thr
			20					25					30	
Ala	Ala	Gln	Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp
			35					40					45	
Cys	Thr	Cys	Asp	Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg
			50					55					60	
Leu	Phe	Pro	Arg	Leu	Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg
			65					70					75	

Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp	80	85	90
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln	95	100	105
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr	110	115	120
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu	125	130	135
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys	140	145	150
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe	155	160	165
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp	170	175	180
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp	185	190	195
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys	200	205	210
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln	215	220	225
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu	230	235	240
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His	245	250	255
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu	260	265	270
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln	275	280	285
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg	290	295	300
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu	305	310	315
Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	320	325	330
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	335	340	345
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	350	355	360
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys			

	365		370		375
Glu Asp Phe Arg	Leu His Phe Arg Asn	Ile Ser Arg Ile Met Asp			
	380	385		390	
Cys Val Gly Cys	Phe Lys Cys Arg Leu	Trp Gly Lys Leu Gln Thr			
	395	400		405	
Gln Gly Leu Gly	Thr Ala Leu Lys Ile	Leu Phe Ser Glu Lys Leu			
	410	415		420	
Ile Ala Asn Met	Pro Glu Ser Gly Pro	Ser Tyr Glu Phe His Leu			
	425	430		435	
Thr Arg Gln Glu	Ile Val Ser Leu Phe	Asn Ala Phe Gly Arg Ile			
	440	445		450	
Ser Thr Ser Val	Lys Glu Leu Glu Asn	Phe Arg Asn Leu Leu Gln			
	455	460		465	

Asn Ile His

<210> 338
 <211> 507
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> unsure
 <222> 101, 263, 376, 397, 426
 <223> unknown base

<400> 338
 gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50
 ttaaaagacc tttaaactct ttggcttctg gtcaaggac aagtgaagag 100
 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200
 caagatatct ttacaagag acctggttag aaaagaaatg gggacacaac 250
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350
 ctttatccaa agtgttacca ttcttngagc gccagattt tcaactnttt 400
 actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450
 acttcatgaa atcaagtcatt ttcctttgca ttttgatgag aattcatttt 500
 tttgctg 507

<210> 339
 <211> 20

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 339
 aagctgccgg agctgcaatg 20

 <210> 340
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 340
 ttgcttctta atcctgagcg c 21

 <210> 341
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 341
 aaaggaggac ttctgactgc 20

 <210> 342
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 342
 agagattcat ccactgctcc aagtcg 26

 <210> 343
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 343
 tgtccagaaa caggcacata tcagc 25

 <210> 344
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 344
agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345
<211> 1486
<212> DNA
<213> Homo sapiens

<400> 345
cggacgcgtg ggcggacgcg tggcgacgcg cgtgggttgg gagggggcag 50
gatgggaggg aaagtgaaga aaacagaaaa ggagaggggac agaggccaga 100
ggactttctca tactggacag aaaccgatca ggcattggaac tccccttcgt 150
cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200
ttaacctgga tgaacatcac ccacgcctat tcccaggggcc accagaagct 250
gaatttggtg acagtgtctt acaacatgtt gggggtggac agcgatggat 300
gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350
tttatcgctg ccctgtaggg ggggcccaaca atgccccatg tgccaagggc 400
cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450
gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500
tgagctaagg agagggtggt ggcagtgtct ctgaagggtcc ataaaagaaa 550
aaagagaagt gtggtgaagg aaaatggtct gtgtggaggg gtcaaggagt 600
taaaaaccct agaaagcaaa aggtaggtaa tgtcaggggag tagtcttcat 650
gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700
gtaactatth ccccatccc caggcctgtg cccctctctg gtctcgtgct 750
tgtggcagct ctgtcttcag ttctgggata tgtgccctgt tggatgcttc 800
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aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900
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cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050
caaggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100
catggtgaaa ctccatctct actaaaaaaa aaaaaataca aaaattagct 1150

gggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200
 ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250
 gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300
 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
 gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
 gcaggaggat tgcttgaggt ctggagggtt gagaccagcc tgggcaacat 1450
 agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 346
 Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe
 1 5 10 15
 Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro
 20 25 30
 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val
 35 40 45
 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala
 50 55 60
 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg
 65 70 75
 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
 80 85 90
 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn
 95 100 105
 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly
 110 115 120
 Phe Met Val Ser

<210> 347
 <211> 509
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 22
 <223> unknown base

<400> 347

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 ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
 ggagagggac agaggccaga ggacttctca tactggacag aaaccgatca 150
 ggcatggaac tccccctcgt cactcacctg ttcttgcccc tgggtgttct 200
 gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
 tcccagggcc accagaagct gaatttggat acagtgtctt acaacatgtt 300
 gggggtggac agcgatggat gctggtgggc gccccctggg atgggccttc 350
 aggcgaccgg aggggggacg tttatcgctg ccctgtaggg gggggccaca 400
 atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
 tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500
 tggatgatgg 509

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 348
 agggacagag gccagaggac ttc 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 349
 caggtgcata ttcacagcag gatg 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 350
 ggaactcccc ttcgtcactc acctgttctt gcccctgggtg ttcct 45

<210> 351
 <211> 2056
 <212> DNA

<213> Homo sapiens

<400> 351

aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50
catctggggtt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100
gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200
gctttatttt ggaaagaaac aatgttctag gtcaaaactga gtctacaaaa 250
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300
tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400
tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500
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atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650
ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc 700
acctggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750
gcctactgga ggaggagacc tggtgccgag gaacatgtca aaatggtgag 800
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850
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ttcagccaga cagaatgtgt ggaggtgcaa ggagaggcca ttcccctggt 950
actggccctg tttgcctttg ttggcttcat gctgatcctt gtggtcgtgc 1000
cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050
gtgggtggtcc tcccagacac cttgaaaata accaattcac cccagaagtt 1100
aatcagctgc agaaggaggg aggtggatgc ctgtgccacg gctgtgatgt 1150
ctcctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200
caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250
aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300
gagcctgttg tctacaagtc tagaagcaac catcagaggc aggggtggtt 1350
gtctaacaga aactgactg aggcttaggg gatgtgacct ctagactggg 1400

ggctgccact tgctggctga gcaaccctgg gaaaagtac ttcattccctt 1450
 cggtcctaag ttttctcatc tgtaatgggg gaattaccta cacacctgct 1500
 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550
 tacaccacgc acttgcaagg ctagagggaa actggtgaca ctctacagtc 1600
 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650
 gatcaaggac tctacacact ggggtggcttg gagagcccac tttcccagaa 1700
 taatccttga gagaaaagga atcatgggag caatggtgtt gagttcactt 1750
 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050
 aaaaaa 2056

<210> 352
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 352
 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu
 1 5 10 15
 Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp
 20 25 30
 Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
 35 40 45
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro
 50 55 60
 Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu
 65 70 75
 Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser
 80 85 90
 Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala
 95 100 105
 Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln
 110 115 120

Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser
				125					130					135
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe
				140					145					150
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe
				155					160					165
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val
				170					175					180
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met
				185					190					195
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys
				200					205					210
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu
				215					220					225
Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe
				230					235					240
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp
				245					250					255
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val
				260					265					270
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile
				275					280					285
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met
				290					295					300
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser				
				305					310					

<210> 353
 <211> 864
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 654, 711, 748, 827
 <223> unknown base

<400> 353
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 cctttctagc ttctgggccg gctctagaac aattcaggct tcgctgacgac 100
 tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150
 agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200

ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250
 tcatgtgggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300
 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
 gcattctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400
 attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450
 tggatcccca gcagctgggtg ctcaactcact gaaggtcctg agtgtgatgt 500
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
 cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600
 agaaaactcaa ccatccttac ccgacctggg atggagatca ccaaagatgg 650
 cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700
 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
 gaacccttg cgcccgctgg ggtatctctc gagaaaagag aggcccaata 800
 tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850
 ggcgctgggt tgat 864

<210> 354
 <211> 23
 <212> DNA
 <213> Artificial Sequence .

<220>
 <223> Synthetic oligonucleotide probe

<400> 354
 aggttcgct gcgactagac ctc 23

<210> 355
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 355
 ccaggtcggg taaggatggt tgag 24

<210> 356
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<400> 356
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA
<213> Homo sapiens

<400> 357
ccccacgctc cgcccacgcy tccgagggac aagagagaag agagactgaa 50
acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100
ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150
agaggcagga gctggaaaagg agagagggag gagggaggag agatgcggga 200
tgagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250
agaggaggtg tgggttagga accaagaggt agccctgttg gcagcagaag 300
gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350
ggaaaagagc agaggaaaaga ggaaagacac agagagacgg gagagagaag 400
aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450
gggaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500
ggacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550
gcgttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600
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agctcacatc ggaccagcac ctgaccccgga ggactggtgg agctacaagg 700
ataatctcca gggaaaacttc gtgccagggc ctcctttctg gggcctgggtg 750
aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gccccgtgga 800
tgtggagctg aagagggttc tttatgaccc ctttctgccc ccattaaggc 850
tcagcactgg aggagagaag ctccggggaa ccttgtacaa caccggccga 900
catgtctcct tcctgcctgc accccgacct gtggtcaatg tgtctggagg 950
tcccctcctt tacagccacc gactcagtga actgcggctg ctgtttggag 1000
ctcgcgacgg agccggctcg gaacatcaga tcaaccacca gggcttctct 1050
gctgaggtgc agctcattca cttcaaccag gaactctacg ggaatttcag 1100
cgctgcctcc cgcggcccca atggcctggc cattctcagc ctctttgtca 1150
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accatcactc gcatctccta caagaatgat gcctactttc ttcaagacct 1250

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gagcctggag ctccctgttcc ctgaatcctt cggcttcac acctatcagg 1300
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gaccgggccc tcaatatcac ctcccttcag atgcactccc tgagactcct 1400
gagccagaat cctccatctc agatcttcca gagcctcagc ggtaacagcc 1450
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cggcaccccg agaggcgctg ccgaggcccc aactaccgcc tgcattgtgga 1550
tgggtgtcccc catggtcgtt gagactcccc ttcgaggatt gcacccgccc 1600
gtcctaagcc tccccacaag gcgaggggag ttaccacctaa aacaaagcta 1650
ttaaaggac agaatactta 1670

<210> 358
<211> 328
<212> PRT
<213> Homo sapiens

<400> 358
Met Gly Ala Ala Ala Arg Leu Ser Ala Pro Arg Ala Leu Val Leu
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Trp Ala Ala Leu Gly Ala Ala Ala His Ile Gly Pro Ala Pro Asp
20 25 30
Pro Glu Asp Trp Trp Ser Tyr Lys Asp Asn Leu Gln Gly Asn Phe
35 40 45
Val Pro Gly Pro Pro Phe Trp Gly Leu Val Asn Ala Ala Trp Ser
50 55 60
Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu
65 70 75
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser
80 85 90
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg
95 100 105
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser
110 115 120
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu
125 130 135
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn
140 145 150
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln
155 160 165
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly

170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn	Val Ala Ser Thr Ser Asn	
185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg	Asp Thr Ile Thr Arg Ile	
200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu	Gln Asp Leu Ser Leu Glu	
215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe	Ile Thr Tyr Gln Gly Ser	
230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr	Val Thr Trp Ile Leu Ile	
245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu	Gln Met His Ser Leu Arg	
260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln	Ile Phe Gln Ser Leu Ser	
275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu	Ala His Arg Ala Leu Arg	
290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu	Arg Arg Cys Arg Gly Pro	
305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val	Pro His Gly Arg	
320	325	

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 359
 tctgctgagg tgcagctcat tcac 24

<210> 360
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 360
 gaggtctgg aagatctgag atgg 24

<210> 361
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 361

gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362

<211> 3038

<212> DNA

<213> Homo sapiens

<400> 362

ggcgcctggg tctgcgcgta ctggctgtac ggagcaggag caagaggtcg 50

ccgccagcct ccgccgccga gcctcgttcg tgtccccgcc cctcgtcct 100

gcagctactg ctcaaaaacg ctggggcgcc caccctggca gactaacgaa 150

gcagctccct tcccacccca actgcaggtc taattttgga cgctttgcct 200

gccatttctt ccagggttgag ggagccgcag aggcggaggc tcgcgtattc 250

ctgcagtcag caccacgctc gccccggac gctcgggtgct caggcccttc 300

gcgagcgggg ctctccgtct gcggtccctt gtgaaggctc tgggcggctg 350

cagaggccgg ccgtccggtt tggctcacct ctcccaggaa acttcacact 400

ggagagccaa aaggagtggg agagcctgtc ttggagattt tcctggggaa 450

atcctgaggt cattcattat gaagtgtacc gcgcgggagt ggctcagagt 500

aaccacagtg ctgttcatgg ctagagcaat tccagccatg gtggttccca 550

atgccacttt attggagaaa ctttttgaaa aatacatgga tgaggatggt 600

gagtgggtgga tagccaaaca acgagggaaa agggccatca cagacaatga 650

catgcagagt attttggacc ttcataataa attacgaagt caggtgtatc 700

caacagcctc taatatggag tatatgacat gggatgtaga gctggaaaga 750

tctgcagaat cctgggctga aagttgcttg tgggaacatg gacctgcaag 800

cttgcttcca tcaattggac agaatttggg agcacttg ggaagatata 850

ggcccccgac gtttcatgta caatcgtggt atgatgaagt gaaagacttt 900

agctacccat atgaacatga atgcaacca tattgtccat tcaggtgttc 950

tggccctgta tgtacacatt atacacaggc cgtgtgggca actagtaaca 1000

gaatcggttg tgccattaat ttgtgtcata acatgaacat ctgggggcag 1050

atatggccca aagctgtcta cctggtgtgc aattactccc caaagggaaa 1100

ctggtggggc catgccccctt acaaacatgg gcggccctgt tctgcttgcc 1150

cacctagttt tggagggggc tgtagagaaa atctgtgcta caaagaaggg 1200
tcagacaggt attatcccc tcgagaagag gaaacaaatg aaatagaacg 1250
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cgaatgtcct gctggctgtt tggatagtaa agctaaagtt attggcagtg 1450
tacattatga aatgcaatcc agcatctgta gagctgcaat tcattatggg 1500
ataatagaca atgatggtag ctgggtagat atcactagac aaggaagaaa 1550
gcattatttc atcaagtcca atagaaatgg tattcaaaca attggcaaatt 1600
atcagttctgc taattccttc acagttctta aagtaacagt tcaggctgtg 1650
acttgtgaaa caactgtgga acagttctgt ccatttcata agcctgtctc 1700
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attatgctcg tgtaattgga actcgagttt attctgatct gtccagtatc 1800
tgcagagcag cagtacatgc tggagtgggt cgaaatcacg gtgggttatgt 1850
tgatgtaatg cctgtggaca aaagaaagac ctacattgct tcttttcaga 1900
atggaatctt ctcagaaagt ttacagaatc ctccaggagg aaaggcattc 1950
agagtgtttg ctgttgtgtg aaactgaata cttggaagag gaccataaag 2000
actattccaa atgcaatatt tctgaatttt gtataaaaact gtaacattac 2050
tgtacagagt acatcaacta ttttcagccc aaaaaggtgc caaatgcata 2100
taaatcttga taaacaaagt ctataaaata aaacatggga cattagcttt 2150
gggaaaagta atgaaaatat aatggtttta gaaatcctgt gttaaattatt 2200
gctatatttt cttagcagtt atttctacag ttaattacat agtcatgatt 2250
gttctacgtt tcatatatta tatgggtgctt tgtatatgcc actaataaaa 2300
tgaatctaaa cattgaatgt gaatggccct cagaaaatca tctagtgcatt 2350
ttaaaaaataa tcgactctaa aactgaaaga aaccttatca cattttcccc 2400
agttcaatgc tatgccatta ccaactccaa ataattctcaa ataattttcc 2450
acttaataac tgtaaagttt ttttctgtta atttaggcat atagaatatt 2500
aaattctgat attgcacttc ttattttata taaaataatc ctttaatatc 2550
caaatgaatc tgttaaaatg tttgattcct tgggaatggc cttaaaaata 2600

aatgtaataa agtcagagtg gtggtatgaa aacattccta gtgatcatgt 2650
agtaaatgta ggggttaagca tggacagcca gagctttcta tgtactgtta 2700
aaattgaggt cacatatattt cttttgtatc ctggcaaata ctcctgcagg 2750
ccaggaagta taatagcaaa aagttgaaca aagatgaact aatgtattac 2800
attaccattg ccactgattt tttttaaatg gtaaatgacc ttgtatataa 2850
atattgccat atcatggtac ctataatggt gatataatttg tttctatgaa 2900
aaatgtattg tgctttgata ctaaaaatct gtaaaatggt agttttggta 2950
attttttttc tgctggtgga tttacatatt aaattttttc tgctggtgga 3000
taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363
<211> 500
<212> PRT
<213> Homo sapiens

<400> 363
Met Lys Cys Thr Ala Arg Glu Trp Leu Arg Val Thr Thr Val Leu
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Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr
20 25 30
Leu Leu Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu
35 40 45
Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn
50 55 60
Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln
65 70 75
Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val
80 85 90
Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp
95 100 105
Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu
110 115 120
Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln
125 130 135
Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His
140 145 150
Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys
155 160 165
Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser Asn Arg Ile Gly

	170	175	180
Cys Ala Ile Asn	Leu Cys His Asn Met	Asn Ile Trp Gly Gln Ile	
	185	190	195
Trp Pro Lys Ala	Val Tyr Leu Val Cys	Asn Tyr Ser Pro Lys Gly	
	200	205	210
Asn Trp Trp Gly	His Ala Pro Tyr Lys	His Gly Arg Pro Cys Ser	
	215	220	225
Ala Cys Pro Pro	Ser Phe Gly Gly Gly	Cys Arg Glu Asn Leu Cys	
	230	235	240
Tyr Lys Glu Gly	Ser Asp Arg Tyr Tyr	Pro Pro Arg Glu Glu Glu	
	245	250	255
Thr Asn Glu Ile	Glu Arg Gln Gln Ser	Gln Val His Asp Thr His	
	260	265	270
Val Arg Thr Arg	Ser Asp Asp Ser Ser	Arg Asn Glu Val Ile Ser	
	275	280	285
Ala Gln Gln Met	Ser Gln Ile Val Ser	Cys Glu Val Arg Leu Arg	
	290	295	300
Asp Gln Cys Lys	Gly Thr Thr Cys Asn	Arg Tyr Glu Cys Pro Ala	
	305	310	315
Gly Cys Leu Asp	Ser Lys Ala Lys Val	Ile Gly Ser Val His Tyr	
	320	325	330
Glu Met Gln Ser	Ser Ile Cys Arg Ala	Ala Ile His Tyr Gly Ile	
	335	340	345
Ile Asp Asn Asp	Gly Gly Trp Val Asp	Ile Thr Arg Gln Gly Arg	
	350	355	360
Lys His Tyr Phe	Ile Lys Ser Asn Arg	Asn Gly Ile Gln Thr Ile	
	365	370	375
Gly Lys Tyr Gln	Ser Ala Asn Ser Phe	Thr Val Ser Lys Val Thr	
	380	385	390
Val Gln Ala Val	Thr Cys Glu Thr Thr	Val Glu Gln Leu Cys Pro	
	395	400	405
Phe His Lys Pro	Ala Ser His Cys Pro	Arg Val Tyr Cys Pro Arg	
	410	415	420
Asn Cys Met Gln	Ala Asn Pro His Tyr	Ala Arg Val Ile Gly Thr	
	425	430	435
Arg Val Tyr Ser	Asp Leu Ser Ser Ile	Cys Arg Ala Ala Val His	
	440	445	450
Ala Gly Val Val	Arg Asn His Gly Gly	Tyr Val Asp Val Met Pro	
	455	460	465

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile
 470 475 480

Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg
 485 490 495

Val Phe Ala Val Val
 500

<210> 364
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 364
 ggacagaatt tgggagcaca ctgg 24

<210> 365
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 365
 ccaagagtat actgtcctcg 20

<210> 366
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 366
 agcacagatt ttctctacag ccccc 25

<210> 367
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 367
 aaccactcca gcatgtactg ctgc 24

<210> 368
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe
 <400> 368
 ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50
 <210> 369
 <211> 1685
 <212> DNA
 <213> Homo sapiens
 <400> 369
 gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50
 ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100
 agagaaaagcc gagcagagct ggggtggcgtc tccgggcccgc cgctccgacg 150
 ggccagcgcc ctccccatgt ccctgctccc acgccgcgcc cctccggtca 200
 gcatgaggct cctggcggcc gcgctgctcc tgctgctgct ggcgctgtac 250
 accgcgcgtg tggacgggtc caaatgcaag tgctcccga agggacccaa 300
 gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgc 350
 actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccaggtag 400
 cgaggtcagg agcactgcct gcaccccaag ctgcagagca ccaagcgctt 450
 catcaagtgg tacaacgcct ggaacgagaa gcgcagggtc tacgaagaat 500
 aggggtgaaaa acctcagaag ggaaaaactcc aaaccagttg ggagacttgt 550
 gcaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600
 aaaaaaaaaa aaagcctttc tttctcacag gcataagaca caaattatat 650
 attgttatga agcacttttt accaacggtc agtttttaca ttttatagct 700
 gcgtgcgaaa ggcttcaga tgggagaccc atctctcttg tgctccagac 750
 ttcacacag gctgcttttt atcaaaaagg ggaaaactca tgcctttcct 800
 ttttaaaaaa tgcttttttg tatttgtcca tacgtcacta tacatctgag 850
 ctttataagc gcccgaggag aacaatgagc ttggtggaca catttcattg 900
 cagtgttgct ccattcctag cttgggaagc ttccgcttag aggtcctggc 950
 gcctcggcac agctgccacg ggctctcctg ggcttatggc cggtcacagc 1000
 ctcagtgtga ctccacagtg gccctgtag ccgggcaagc aggagcaggt 1050
 ctctctgcat ctgttctctg aggaactcaa gtttggttgc cagaaaaatg 1100
 tgcttcattc cccctggtt aatttttaca caccctagga aacatttcca 1150

agatcctgtg atggcgagac aaatgaccc taaagaaggt gtgggggtctt 1200
 tcccaacctg aggatttctg aaagggtcac aggttcaata tttaatgctt 1250
 cagaagcatg tgagggtccc aacactgtca gcaaaaacct taggagaaaa 1300
 cttaaaaaata tatgaatata tgcgcaatac acagctacag acacacattc 1350
 tggtgacaag ggaaaacctt caaagcatgt ttctttccct caccacaaca 1400
 gaacatgcag tactaaagca atatatttgt gattcccat gtaattcttc 1450
 aatgttaaac agtgagctcc tctttcgaaa gctaagatga ccatgcgccc 1500
 tttcctctgt acatataccc ttaagaacgc cccctccaca cactgcccc 1550
 cagtatatgc cgcattgtac tgctgtgtta tatgctatgt acatgtcaga 1600
 aaccattagc attgcatgca ggtttcatat tctttctaag atggaaagta 1650
 ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 370
 Met Ser Leu Leu Pro Arg Arg Ala Pro Pro Val Ser Met Arg Leu
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 20 25 30
 Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys
 35 40 45
 Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
 50 55 60
 Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val
 65 70 75
 Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln
 80 85 90
 Ser Thr Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys
 95 100 105
 Arg Arg Val Tyr Glu Glu
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 <213> Artificial Sequence
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<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

ctccggtcag catgaggctc ctggcgcccg ctgctcctgc tgctg 45

<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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tggttaaactc caatgtcctc ctgtgggttaa ctgctcttgc catcaagttc 100

accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150

caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200

tggagcagta cttaggggtc ccctatgcct cccccccac tggagagagg 250

cggtttcagc cccagaacc cccgtcctcc tggactggca tccgaaatac 300

tactcagttt gctgctgtgt gccccagca cctggatgag agatccttac 350

tgcatgacat gctgcccac tggtttaccg ccaatttgga tactttgatg 400

acctatgttc aagatcaaaa tgaagactgc ctttacttaa acatctacgt 450

gcccacggaa gatggagcca acacaaagaa aaacgcagat gatataacga 500

gtaatgaccg tgggtgaagac gaagatattc atgatcagaa cagtaagaag 550

cccgatcatgg tctatatcca tgggggatct tacatggagg gcaccggcaa 600

catgattgac ggcagcattt tggcaagcta cggaacgctc atcgtgatca 650

ccattaacta ccgtctggga atactagggg ttttaagtac cggtgaccag 700
gcagcaaaag gcaactatgg gctcctggat cagattcaag cactgcggtg 750
gattgaggag aatgtgggag cctttggcgg ggacccaag agagtgacca 800
tctttggctc gggggctggg gcctcctgtg tcagcctgtt gaccctgtcc 850
cactactcag aaggtctctt ccagaaggcc atcattcaga gcggcaccgc 900
cctgtccagc tgggcagtga actaccagcc ggccaagtac actcggatat 950
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<210> 375
<211> 816
<212> PRT
<213> Homo sapiens

<400> 375
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Lys Phe Thr Leu Ile Asp Ser Gln Ala Gln Tyr Pro Val Val Asn
20 25 30
Thr Asn Tyr Gly Lys Ile Arg Gly Leu Arg Thr Pro Leu Pro Asn
35 40 45
Glu Ile Leu Gly Pro Val Glu Gln Tyr Leu Gly Val Pro Tyr Ala

				50					55					60
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro
				65					70					75
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val
				80					85					90
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu
				95					100					105
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val
				110					115					120
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro
				125					130					135
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr
				140					145					150
Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser
				155					160					165
Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu
				170					175					180
Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly
				185					190					195
Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly
				200					205					210
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu
				215					220					225
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly
				230					235					240
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly
				245					250					255
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser
				260					265					270
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu
				275					280					285
Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile
				290					295					300
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met
				305					310					315
Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln
				320					325					330
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile
				335					340					345

Asp Gly Asp Val	Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu	Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys	Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn	Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly	Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met	Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu	425	430	435
Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn			

	635		640		645
Asn Pro Lys His	Ser Lys Asp Pro His	Lys Thr Gly Pro Glu	Asp		
	650	655	660		
Thr Thr Val Leu	Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu	Leu		
	665	670	675		
Ser Val Thr Ile	Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn	Ile		
	680	685	690		
Leu Ala Phe Ala	Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg	His		
	695	700	705		
Glu Thr His Arg	Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn	Asp		
	710	715	720		
Ile Ala His Ile	Gln Asn Glu Glu Ile	Met Ser Leu Gln Met	Lys		
	725	730	735		
Gln Leu Glu His	Asp His Glu Cys Glu	Ser Leu Gln Ala His	Asp		
	740	745	750		
Thr Leu Arg Leu	Thr Cys Pro Pro Asp	Tyr Thr Leu Thr Leu	Arg		
	755	760	765		
Arg Ser Pro Asp	Asp Ile Pro Leu Met	Thr Pro Asn Thr Ile	Thr		
	770	775	780		
Met Ile Pro Asn	Thr Leu Thr Gly Met	Gln Pro Leu His Thr	Phe		
	785	790	795		
Asn Thr Phe Ser	Gly Gly Gln Asn Ser	Thr Asn Leu Pro His	Gly		
	800	805	810		
His Ser Thr Thr	Arg Val				
	815				

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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 376
 ggcaagctac ggaaacgtca tcgtg 25

<210> 377
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

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ggccgcatg g 2461

<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

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Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu
20 25 30

Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly
35 40 45

Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu Ser Lys Pro
50 55 60

Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu Met
65 70 75

Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp
80 85 90

Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe
95 100 105

Leu Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln
110 115 120

Gly Lys Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr
125 130 135

Lys Asp Arg Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys
140 145 150

Phe Val Gly Leu Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu
155 160 165

Lys Gln Gln Glu Arg Val Phe Pro Tyr Ile Ser Ala Met Val Asn
170 175 180

Asn Gly Ser Leu Ser Tyr Asp His Glu Arg Asp Gly Arg Pro Thr
185 190 195

Glu Leu Gly Gly Cys Thr Ala Ile Val Arg Asn Leu His Tyr Asp
200 205 210

Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile Met
215 220 225

Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val
230 235 240

Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser
245 250 255

Ile Thr Gly Asp	Leu Ser Asp Asn His	Asp Val Ile Ser Leu	Lys
260		265	270
Leu Phe Glu Leu Thr Val Glu Arg Thr	Pro Glu Glu Glu Lys	Leu	
275	280		285
His Arg Asp Val Phe Leu Pro Ser Val	Asp Asn Met Lys Leu	Pro	
290	295		300
Glu Met Thr Ala Pro Leu Pro Pro Leu	Ser Gly Leu Ala Leu	Phe	
305	310		315
Leu Ile Val Phe Phe Ser Leu Val Phe	Ser Val Phe Ala Ile	Val	
320	325		330
Ile Gly Ile Ile Leu Tyr Asn Lys Trp	Gln Glu Gln Ser Arg	Lys	
335	340		345

Arg Phe Tyr

<210> 381
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 382
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 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 382
 cactctccag gctgcatgct cagg 24

<210> 383
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 383
 gtcaaacgtt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384
 <211> 3150
 <212> DNA
 <213> Homo sapiens

<400> 384

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 ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150
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 tgaattgctt ggtacaaaat ggccagttca cagaggaata gaaggactt 1950
 tatcatagcc agacttcgct tagaatgcca gaataatata gttcaagacc 2000
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 ttctgaagca ggaaagccac cacagacagt acataaagga atatgtgtag 2300
 ctgggttccc aggccagaca aaacagatgg tgaccagact tggcccctgg 2350
 gctgtagttt gctgaccct catctaaaaa ataggctata ctacaattgc 2400
 actccagca ctttgagaac gagttgaata ccaagaatta ttcaatgggt 2450
 cctccagtaa cttctgctag aaacacagaa tttggtctgt atctgacact 2500
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 actggattca tttttaaac attttcatca gtttcaaag gttaaattctg 2900

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 tgatttctga actaatgggtg ctaattcaga gaaatggaaa gtgaaagtga 3050
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<210> 385
 <211> 480
 <212> PRT
 <213> Homo sapiens

<400> 385
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 Pro Val Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys
 35 40 45
 Arg Ile Met Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro
 50 55 60
 Val Tyr Glu Ala Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu
 65 70 75
 Arg Ser Met Glu Gly His Ala Pro His His Phe Lys Leu Val Ser
 80 85 90
 Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro Leu Tyr Val
 95 100 105
 Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu Val Ala
 110 115 120
 Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser His
 125 130 135
 Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser
 140 145 150
 Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu
 155 160 165
 Thr Gln Thr Gly Val Val Gln His Leu Gln Asn Gly Gln Leu Leu
 170 175 180
 Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro Asn Asp Trp
 185 190 195
 Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg Thr
 200 205 210

Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe	
				215					220					225	
Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe	
				230					235					240	
Cys	Ser	Gly	Ser	Cys	Tyr	Cys	Pro	Val	Arg	Asn	Gln	Tyr	Leu	Glu	
				245					250					255	
Lys	Glu	Gln	Arg	Arg	Gln	Tyr	Leu	Leu	Arg	Leu	Lys	Asn	Ser	Gln	
				260					265					270	
Leu	Glu	Lys	Thr	Tyr	Gly	Glu	Met	Ala	Lys	Ile	Val	Asp	Val	Pro	
				275					280					285	
Thr	Lys	Gln	Leu	Arg	Ala	Ala	Asn	Pro	Ile	Asp	Ser	Met	Leu	Cys	
				290					295					300	
His	Phe	Cys	His	Asn	Val	Ser	Phe	Pro	Cys	Thr	Arg	Asn	Gly	Cys	
				305					310					315	
Val	Asp	Met	Glu	His	Phe	Lys	Val	Ile	Lys	Thr	His	Gln	Ile	Glu	
				320					325					330	
Asp	Glu	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Leu	Tyr	Phe	Gly	Tyr	Ser	
				335					340					345	
Leu	Leu	Gly	Ala	His	Pro	Ile	Leu	Asn	Gln	Thr	Ile	Gly	Arg	Met	
				350					355					360	
Gln	Arg	Ala	Thr	Glu	Gly	Arg	Lys	Glu	Glu	Leu	Phe	Ala	Leu	Tyr	
				365					370					375	
Ser	Ala	His	Asp	Val	Thr	Leu	Ser	Pro	Val	Leu	Ser	Ala	Leu	Gly	
				380					385					390	
Leu	Ser	Glu	Ala	Arg	Phe	Pro	Arg	Phe	Ala	Ala	Arg	Leu	Ile	Phe	
				395					400					405	
Glu	Leu	Trp	Gln	Asp	Arg	Glu	Lys	Pro	Ser	Glu	His	Ser	Val	Arg	
				410					415					420	
Ile	Leu	Tyr	Asn	Gly	Val	Asp	Val	Thr	Phe	His	Thr	Ser	Phe	Cys	
				425					430					435	
Gln	Asp	His	His	Lys	Arg	Ser	Pro	Lys	Pro	Met	Cys	Pro	Leu	Glu	
				440					445					450	
Asn	Leu	Val	Arg	Phe	Val	Lys	Arg	Asp	Met	Phe	Val	Ala	Leu	Gly	
				455					460					465	
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 386
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<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 387
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<210> 388
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 388
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<210> 389
<211> 3313
<212> DNA
<213> Homo sapiens

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cacgcgcctg aagcacaaaag cagatagcta ggaatgaacc atccctggga 250
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 aaactctatc tca 3313

<210> 390
 <211> 916
 <212> PRT
 <213> Homo sapiens
 <400> 390

09978187-101501

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				20					25					30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	
				35					40					45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	
				50					55					60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	
				65					70					75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	
				80					85					90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	
				95					100					105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	
				110					115					120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	
				125					130					135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	
				140					145					150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	
				155					160					165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	
				170					175					180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	
				185					190					195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	
				200					205					210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	
				215					220					225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	
				230					235					240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	
				245					250					255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	
				260					265					270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	
				275					280					285	
Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr	

	290		295		300
Ile Ser Thr Ile	Gly 305	Glu Leu Asp His	Glu 310	Glu Ser Gly Phe	Tyr 315
Gln Met Glu Val	Gln 320	Ala Met Asp Asn	Ala 325	Gly Tyr Ser Ala	Arg 330
Ala Lys Val Leu	Ile 335	Thr Val Leu Asp	Val 340	Asn Asp Asn Ala	Pro 345
Glu Val Val Leu	Thr 350	Ser Leu Ala Ser	Ser 355	Val Pro Glu Asn	Ser 360
Pro Arg Gly Thr	Leu 365	Ile Ala Leu Leu	Asn 370	Val Asn Asp Gln	Asp 375
Ser Glu Glu Asn	Gly 380	Gln Val Ile Cys	Phe 385	Ile Gln Gly Asn	Leu 390
Pro Phe Lys Leu	Glu 395	Lys Ser Tyr Gly	Asn 400	Tyr Tyr Ser Leu	Val 405
Thr Asp Ile Val	Leu 410	Asp Arg Glu Gln	Val 415	Pro Ser Tyr Asn	Ile 420
Thr Val Thr Ala	Thr 425	Asp Arg Gly Thr	Pro 430	Pro Leu Ser Thr	Glu 435
Thr His Ile Ser	Leu 440	Asn Val Ala Asp	Thr 445	Asn Asp Asn Pro	Pro 450
Val Phe Pro Gln	Ala 455	Ser Tyr Ser Ala	Tyr 460	Ile Pro Glu Asn	Asn 465
Pro Arg Gly Val	Ser 470	Leu Val Ser Val	Thr 475	Ala His Asp Pro	Asp 480
Cys Glu Glu Asn	Ala 485	Gln Ile Thr Tyr	Ser 490	Leu Ala Glu Asn	Thr 495
Ile Gln Gly Ala	Ser 500	Leu Ser Ser Tyr	Val 505	Ser Ile Asn Ser	Asp 510
Thr Gly Val Leu	Tyr 515	Ala Leu Ser Ser	Phe 520	Asp Tyr Glu Gln	Phe 525
Arg Asp Leu Gln	Val 530	Lys Val Met Ala	Arg 535	Asp Asn Gly His	Pro 540
Pro Leu Ser Ser	Asn 545	Val Ser Leu Ser	Leu 550	Phe Val Leu Asp	Gln 555
Asn Asp Asn Ala	Pro 560	Glu Ile Leu Tyr	Pro 565	Ala Leu Pro Thr	Asp 570
Gly Ser Thr Gly	Val 575	Glu Leu Ala Pro	Arg 580	Ser Ala Glu Pro	Gly 585

Tyr	Leu	Val	Thr	Lys	Val	Val	Ala	Val	Asp	Arg	Asp	Ser	Gly	Gln	590	595	600
Asn	Ala	Trp	Leu	Ser	Tyr	Arg	Leu	Leu	Lys	Ala	Ser	Glu	Pro	Gly	605	610	615
Leu	Phe	Ser	Val	Gly	Leu	His	Thr	Gly	Glu	Val	Arg	Thr	Ala	Arg	620	625	630
Ala	Leu	Leu	Asp	Arg	Asp	Ala	Leu	Lys	Gln	Ser	Leu	Val	Val	Ala	635	640	645
Val	Gln	Asp	His	Gly	Gln	Pro	Pro	Leu	Ser	Ala	Thr	Val	Thr	Leu	650	655	660
Thr	Val	Ala	Val	Ala	Asp	Ser	Ile	Pro	Gln	Val	Leu	Ala	Asp	Leu	665	670	675
Gly	Ser	Leu	Glu	Ser	Pro	Ala	Asn	Ser	Glu	Thr	Ser	Asp	Leu	Thr	680	685	690
Leu	Tyr	Leu	Val	Val	Ala	Val	Ala	Ala	Val	Ser	Cys	Val	Phe	Leu	695	700	705
Ala	Phe	Val	Ile	Leu	Leu	Leu	Ala	Leu	Arg	Leu	Arg	Arg	Trp	His	710	715	720
Lys	Ser	Arg	Leu	Leu	Gln	Ala	Ser	Gly	Gly	Gly	Leu	Thr	Gly	Ala	725	730	735
Pro	Ala	Ser	His	Phe	Val	Gly	Val	Asp	Gly	Val	Gln	Ala	Phe	Leu	740	745	750
Gln	Thr	Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Thr	Asp	Ser	Arg	Lys	755	760	765
Ser	His	Leu	Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Met	Leu	Val	770	775	780
Ser	Gln	Glu	Ser	Phe	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Leu	Ser	Gly	785	790	795
Asp	Ser	Val	Phe	Ser	Lys	Asp	Ser	His	Gly	Leu	Ile	Glu	Val	Ser	800	805	810
Leu	Tyr	Gln	Ile	Phe	Phe	Leu	Phe	Phe	Phe	Asn	Cys	Ser	Val	Ser	815	820	825
Gln	Ala	Gly	Val	Gln	Arg	Tyr	Asp	His	Ser	Ser	Leu	Arg	Pro	Gln	830	835	840
Thr	Pro	Arg	Leu	Lys	Gln	Leu	Ser	His	Leu	Cys	Leu	Arg	Cys	Asn	845	850	855
Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr	860	865	870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu			

09978187.101501

875					880					885				
Ser	Cys	Thr	Asp	Gly	Ser	Leu	Thr	Pro	Val	Ile	Pro	Val	Leu	Trp
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<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

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<223> Synthetic oligonucleotide probe

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<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

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ggggcctcct ccaactgggtc cgaatcagta ggtgaccccg cccctggatt 150

ctggaagacc tcaccatggg acgccccga cctcgtgctg ccaagacgtg 200

gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250
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<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

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			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75
Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn
			80						85					90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro
			95						100					105

His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp
				110					115					120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys
				125					130					135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln
				140					145					150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu
				155					160					165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro
				170					175					180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly
				185					190					195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly
				200					205					210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile
				215					220					225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly
				230					235					240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile
				245					250					255
Ile	Gly	Ser	Lys	Gly										
				260										

<210> 396
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 396
 cagcctacag aataaagatg gccc 24

<210> 397
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 397
 ggtgcaatga tctgccaggc tgat 24

<210> 398
 <211> 48
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccaccccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

ggcgccggtg caccgggagg gctgagcgcc tcctgcggcc cggcctgcgc 50
gccccggccc gccgcggcgc ccacgccccca accccggccc gcgcccccta 100
gccccgcgcc gggcccgccg ccgcgccccg gccaggtga gcgctccgcc 150
cgccgcgagg ccccgccccg gcccgccccg gccccgcccc ggccggcggg 200
ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250
tcctcctccc ggcgggccgc gctgcgagcg ccccgccagt ccgcgcccgc 300
gccgcccctg ccctgtgcgc cctgcgcgcc ctgcgcaccc gcggccccgag 350
cccagccaga gccgggaggga gcggagcgcg ccgagcctcg tcccgcggcc 400
gggcccgggc cgggcccgtg cggcgggcgc tggatgcgga cccggcccgc 450
gggagacggg cgcccgcccc gaaacgactt tcagtccccg acgcgccccg 500
cccaaccctt acgatgaaga gggcgtccgc tggagggagc cggctgctgg 550
catgggtgct gtggctgcag gcctggcagg tggcagcccc atgcccaggt 600
gcctgcgtat gctacaatga gccaagggtg acgacaagct gccccagca 650
gggcctgcag gctgtgcccg tgggcatccc tgctgccagc cagcgcatct 700
tcctgcacgg caaccgcacg tcgcatgtgc cagctgccag cttccgtgcc 750
tgccgcaacc tcaccatcct gtggctgcac tcgaatgtgc tggcccgaat 800
tgatgcggct gccttcaact gcctggccct cctggagcag ctggacctca 850
gcgataatgc acagctccgg tctgtggacc ctgccacatt ccacggcctg 900
ggccgcctac acacgctgca cctggaccgc tgcggcctgc aggagctggg 950
cccggggctg ttccgcggcc tggctgccct gcagtacctc tacctgcagg 1000
acaacgcgct gcaggcactg cctgatgaca cttccgcga cctgggcaac 1050
ctcacacacc tcttcctgca cggcaaccgc atctccagcg tgcccagcgc 1100

cgcttccgt gggctgcaca gcctcgaccg tctcctactg caccagaacc 1150
 gcgtggccca tgtgcacccg catgccttcc gtgaccttgg ccgcctcatg 1200
 acactctatc tgtttgccaa caatctatca gcgctgccca ctgaggccct 1250
 ggccccctg cgtgccctgc agtacctgag gctcaacgac aaccctggg 1300
 tgtgtgactg ccggggcacgc ccactctggg cctgggtgca gaagttccgc 1350
 ggctcctcct ccgaggtgcc ctgcagcctc ccgcaacgcc tggctggccg 1400
 tgacctcaaa cgcttagctg ccaatgacct gcaggggtgc gctgtggcca 1450
 ccggccctta ccatcccatc tggaccggca gggccaccga tgaggagccg 1500
 ctggggcttc ccaagtgtg ccagccagat gccgctgaca aggcctcagt 1550
 actggagcct ggaagaccag cttcggcagg caatgcgctg aagggacgcg 1600
 tgccgcccgg tgacagcccg ccgggcaacg gctctggccc acggcacatc 1650
 aatgactcac cctttgggac tctgcctggc tctgctgagc ccccgctcac 1700
 tgcaagtgcg cccgagggct ccgagccacc agggttcccc acctcgggcc 1750
 ctgcgccggag gccaggctgt tcacgcaaga accgcacccg cagccactgc 1800
 cgtctggggc aggcaggcag cgggggtggc gggactggtg actcagaagg 1850
 ctcaggtgcc ctaccagcc tcacctgcag cctcaccccc ctgggcctgg 1900
 cgctggtgct gtggacagt cttgggccct gctgaccccc agcggacaca 1950
 agagcgtgct cagcagccag gtgtgtgtac atacggggtc tctctccacg 2000
 ccgccaagcc agccgggcg ccgaccctg gggcaggcca ggccaggtcc 2050
 tccctgatgg acgcctgccg cccgccaccc ccattctccac cccatcatgt 2100
 ttacaggggt cggcggcagc gtttgttcca gaacgccgcc tcccaccag 2150
 atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200
 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400
 <211> 473
 <212> PRT
 <213> Homo sapiens

<400> 400
 Met Lys Arg Ala Ser Ala Gly Gly Ser Arg Leu Leu Ala Trp Val
 1 5 10 15
 Leu Trp Leu Gln Ala Trp Gln Val Ala Ala Pro Cys Pro Gly Ala
 20 25 30

Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	35	40	45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	50	55	60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	65	70	75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	80	85	90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	95	100	105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	110	115	120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	125	130	135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	140	145	150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	155	160	165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	170	175	180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	185	190	195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	200	205	210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	215	220	225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	230	235	240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	245	250	255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	260	265	270
Leu	Trp	Ala	Trp	Leu	Gln	Lys	Phe	Arg	Gly	Ser	Ser	Ser	Glu	Val	275	280	285
Pro	Cys	Ser	Leu	Pro	Gln	Arg	Leu	Ala	Gly	Arg	Asp	Leu	Lys	Arg	290	295	300
Leu	Ala	Ala	Asn	Asp	Leu	Gln	Gly	Cys	Ala	Val	Ala	Thr	Gly	Pro	305	310	315
Tyr	His	Pro	Ile	Trp	Thr	Gly	Arg	Ala	Thr	Asp	Glu	Glu	Pro	Leu			

	320		325		330
Gly Leu Pro Lys	Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala	Ser		
	335		340		345
Val Leu Glu Pro	Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu	Lys		
	350		355		360
Gly Arg Val Pro	Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser	Gly		
	365		370		375
Pro Arg His Ile	Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly	Ser		
	380		385		390
Ala Glu Pro Pro	Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu	Pro		
	395		400		405
Pro Gly Phe Pro	Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys	Ser		
	410		415		420
Arg Lys Asn Arg	Thr Arg Ser His Cys	Arg Leu Gly Gln Ala	Gly		
	425		430		435
Ser Gly Gly Gly	Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala	Leu		
	440		445		450
Pro Ser Leu Thr	Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu	Val		
	455		460		465
Leu Trp Thr Val	Leu Gly Pro Cys				
	470				

<210> 401
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 401
 tggtgacct gcagtacctc tacc 24

<210> 402
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 402
 ccctgcaggt cattggcagc tagg 24

<210> 403
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe
 <400> 403
 aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404
 <211> 2738
 <212> DNA
 <213> Homo sapiens

<400> 404
 ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50
 ggagaggact actcactggc atattttctga ggtatctgta gaataaccac 100
 agcctcagat actgggggact ttacagtccc acagaaccgt cctcccagga 150
 agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200
 caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250
 cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300
 cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350
 tccaggcggg gggttagggt tgtttccaga ggaacaaac tacatttgca 400
 gctcaatcag gagaccgagg atttggtgct aaatgagaaa ttggaccgtg 450
 aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500
 ctagagagtc ccttcgagtt ttttcaagct gagctgcaag taatagacat 550
 aaacgaccac tctccagtat ttctggacaa acaaagtgtg gtgaaagtat 600
 cagagagcag tcctcctggg actacgtttc ctctgaagaa tgccgaagac 650
 ttagatgtag gccaaaacaa tattgagaac tatataatca gcccactc 700
 ctattttcgg gtcctcaccc gcaaacgcag tgatggcagg aaatacccag 750
 agctggtgct ggacaaagcg ctggaccgag aggaagaagc tgagctcagg 800
 ttaacactca cagcactgga tgggtggtct cgcgccagat ctggcactgc 850
 tcaggtctac atcgaagtcc tggatgtcaa cgataatgcc cctgaatttg 900
 agcagccttt ctatagagtg cagatctctg aggacagtcc ggtaggcttc 950
 ctgggttgta aggtctctgc cacggatgta gacacaggag tcaacggaga 1000
 gatttcctat tcacttttcc aagcttcaga agagattggc aaaaccttta 1050
 agatcaatcc cttgacagga gaaattgaac taaaaaaca actcgatttc 1100
 gaaaaacttc agtcctatga agtcaatatt gaggcaagag atgctggaac 1150

cttttctgga aaatgcaccg ttctgattca agtgatagat gtgaacgacc 1200
atgccccaga agttaccatg tctgcattta ccagcccaat acctgagaac 1250
gcgcctgaaa ctgtggttgc acttttccagt gtttcagatc ttgattcagg 1300
agaaaaatggg aaaattagtt gctccattca ggaggatcta cccttcctcc 1350
tgaaatccgc ggaaaacttt tacaccctac taacggagag accactagac 1400
agagaaagca gagcgggaata caacatcact atcactgtca ctgacttggg 1450
gacccttatg ctgataacac agctcaatat gaccgtgctg atcgccgatg 1500
tcaatgacaa cgctcccgc ttcacccaaa cctcctacac cctgttcgtc 1550
cgcgagaaca acagccccgc cctgcacatc cgcagcgtca gcgctacaga 1600
cagagactca ggcaccaacg ccaggtcac ctactcgtg ctgccgccc 1650
aggacccgca cctgcccctc acatccctgg tctccatcaa cgcggacaac 1700
ggccacctgt tcgccctcag gtctctggac tacgaggccc tgcaggggtt 1750
ccagttccgc gtgggcgctt cagaccacgg ctccccggcg ctgagcagcg 1800
aggcgtggt gcgcgtggtg gtgctggacg ccaacgacaa ctgcccttc 1850
gtgctgtacc cgctgcagaa cggctccgcg ccctgcaccg agctggtgcc 1900
ccgggcggcc gagccgggct acctggtgac caaggtggtg gcggtggacg 1950
gcgactcggg ccagaacgcc tggctgtcgt accagctgct caaggccacg 2000
gagctcggtc tgttcggcgt gtgggcgcac aatggcgagg tgcgcaccgc 2050
caggctgctg agcgagcgcg acgcggccaa gcacaggctg gtggtgctgg 2100
tcaaggacaa tggcgagcct ccgcgtcgg ccaccgccac gctgcacgtg 2150
ctcctggtgg acggcttctc ccagccctac ctgcctctcc cggaggcggc 2200
cccgaccag gccagggcgc acttgctcac cgtctacctg gtggtggcgt 2250
tggcctcggg gtcttcgctc ttctctttt cggctgctct gtctgtggcg 2300
gtgcggctgt gtaggaggag cagggcggcc tcggtgggtc gctgcttgg 2350
gcccgagggc ccccttcag ggcatttgt ggacatgagc ggcaccagga 2400
ccctatccca gagctaccag tatgaggtgt gtctggcagg aggctcagg 2450
accaatgagt tcaagttcct gaagccgatt atcccaact tccctccca 2500
gtgccctggg aaagaaatac aaggaaattc taccttcccc aataactttg 2550
ggttcaatat tcagtacca tagttgactt ttacattcca taggtatttt 2600

attttgtggc atttccatgc caatgtttat ttcccccaat ttgtgtgtat 2650
gtaatattgt acggatttac tcttgatttt tctcatgttc tttctccctt 2700
tgtttttaaag tgaacattta cctttattcc tggttctt 2738

<210> 405
<211> 798
<212> PRT
<213> Homo sapiens

<400> 405
Met Glu Ala Ser Gly Lys Leu Ile Cys Arg Gln Arg Gln Val Leu
1 5 10 15
Phe Ser Phe Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu
20 25 30
Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe
35 40 45
Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe
50 55 60
Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His
65 70 75
Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys
80 85 90
Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu
95 100 105
Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala
110 115 120
Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu
125 130 135
Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly
140 145 150
Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln
155 160 165
Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg
170 175 180
Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu
185 190 195
Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg
200 205 210
Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly
215 220 225
Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala

230	235	240
Pro Glu Phe Glu Gln	Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp	
245	250	255
Ser Pro Val Gly Phe Leu Val Val Lys	Val Ser Ala Thr Asp Val	
260	265	270
Asp Thr Gly Val Asn Gly Glu Ile Ser	Tyr Ser Leu Phe Gln Ala	
275	280	285
Ser Glu Glu Ile Gly Lys Thr Phe Lys	Ile Asn Pro Leu Thr Gly	
290	295	300
Glu Ile Glu Leu Lys Lys Gln Leu Asp	Phe Glu Lys Leu Gln Ser	
305	310	315
Tyr Glu Val Asn Ile Glu Ala Arg Asp	Ala Gly Thr Phe Ser Gly	
320	325	330
Lys Cys Thr Val Leu Ile Gln Val Ile	Asp Val Asn Asp His Ala	
335	340	345
Pro Glu Val Thr Met Ser Ala Phe Thr	Ser Pro Ile Pro Glu Asn	
350	355	360
Ala Pro Glu Thr Val Val Ala Leu Phe	Ser Val Ser Asp Leu Asp	
365	370	375
Ser Gly Glu Asn Gly Lys Ile Ser Cys	Ser Ile Gln Glu Asp Leu	
380	385	390
Pro Phe Leu Leu Lys Ser Ala Glu Asn	Phe Tyr Thr Leu Leu Thr	
395	400	405
Glu Arg Pro Leu Asp Arg Glu Ser Arg	Ala Glu Tyr Asn Ile Thr	
410	415	420
Ile Thr Val Thr Asp Leu Gly Thr Pro	Met Leu Ile Thr Gln Leu	
425	430	435
Asn Met Thr Val Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro Ala	
440	445	450
Phe Thr Gln Thr Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn Ser	
455	460	465
Pro Ala Leu His Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp Ser	
470	475	480
Gly Thr Asn Ala Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln Asp	
485	490	495
Pro His Leu Pro Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp Asn	
500	505	510
Gly His Leu Phe Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu Gln	
515	520	525

Gly Phe Gln Phe Arg Val Gly Ala Ser Asp His Gly Ser Pro Ala	530	535	540
Leu Ser Ser Glu Ala Leu Val Arg Val Val Val Leu Asp Ala Asn	545	550	555
Asp Asn Ser Pro Phe Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala	560	565	570
Pro Cys Thr Glu Leu Val Pro Arg Ala Ala Glu Pro Gly Tyr Leu	575	580	585
Val Thr Lys Val Val Ala Val Asp Gly Asp Ser Gly Gln Asn Ala	590	595	600
Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Leu Gly Leu Phe	605	610	615
Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg Leu Leu	620	625	630
Ser Glu Arg Asp Ala Ala Lys His Arg Leu Val Val Leu Val Lys	635	640	645
Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu His Val	650	655	660
Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu	665	670	675
Ala Ala Pro Thr Gln Ala Gln Ala Asp Leu Leu Thr Val Tyr Leu	680	685	690
Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val	695	700	705
Leu Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala	710	715	720
Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His	725	730	735
Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln	740	745	750
Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys	755	760	765
Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly	770	775	780
Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe	785	790	795
Asn Ile Gln			

<210> 406

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 406
ctgagaacgc gcctgaaact gtg 23

<210> 407
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 407
agcgttgtca ttgacatcgg cg 22

<210> 408
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 408
ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409
<211> 1379
<212> DNA
<213> Homo sapiens

<400> 409
accacgcgt ccgcccacgc gtccgcccac gcgtccgccc acgcgtccgc 50
gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggctgc 100
cggtcgacga ccgccccgcg tcatgcggct cctcggctgg tggcaagtat 150
tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200
agtggtcgct tatggtcaga ggagcagcct gctcaccctc tccaggtggg 250
ggctgtgtac ctgggtgagg aggagctcct gcatgaccgc atgggcccagg 300
acagggcagc agaagaggcc aatgcggtgc tggggctgga caccgaaggc 350
gatcacatgg tgatgctgct tgtgattcct ggggaagctg aggacaaagt 400
gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450
caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500

cacttccctg acagagaaga ggagtattac acagagccag aagtggcggg 550
atctgacgca gccccgacag aggactccaa taacactgaa agtctgaaat 600
cccaaagggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650
actctgaaaa ttttaaataat gtcacaggac cttatggatt ttctgaaccc 700
aaacggtagt gactgtactc tagtcctggt ttacaccccg tgggtgccgt 750
tttctgccag tttggcccct cactttaact ctctgccccg ggcattttcca 800
gctcttcact ttttggcact ggatgcatct cagcacagca gcctttctac 850
cagggtttggc accgtagctg ttcctaataat tttattatit caaggagcta 900
aaccaatggc cagatttaat catacagatc gaacactgga aacactgaaa 950
atctttcattt ttaatcagac aggtatagaa gccaagaaga atgtgggtggt 1000
aactcaagcc gaccaaataag gccctcttcc cagcactttg ataaaaagtg 1050
tggactgggt gcttgtatit tcttattct ttttaattag ttttattatg 1100
tatgtacca ttcgaaactga gagtattcgg tggctaattc caggacaaga 1150
gcaggaacat gtggagtagt gatggtctga aagaagttgg aaagaggaac 1200
ttcaatcctt cgtttcagaa attagtgcata cagtttcata cattttctcc 1250
agtgcgtgt tgacttgaaa cttcaggcag attaaaagaa tcatttggtg 1300
aacaactgaa tgtataaaaa aattataaac tgggtgtttta actagtattg 1350
caataagcaa atgcaaaaat attcaatag 1379

<210> 410
<211> 360
<212> PRT
<213> Homo sapiens

<400> 410
Met Val Pro Ala Ala Gly Arg Arg Pro Pro Arg Val Met Arg Leu
1 5 10 15
Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu Pro Val
20 25 30
Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser Glu
35 40 45
Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly
50 55 60
Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala
65 70 75
Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His

80										85					90				
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val					
				95					100					105					
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu					
				110					115					120					
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly					
				125					130					135					
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu					
				140					145					150					
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn					
				155					160					165					
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg					
				170					175					180					
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met					
				185					190					195					
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys					
				200					205					210					
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser					
				215					220					225					
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu					
				230					235					240					
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr					
				245					250					255					
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly					
				260					265					270					
Ala	Lys	Pro	Met	Ala	Arg	Phe	Asn	His	Thr	Asp	Arg	Thr	Leu	Glu					
				275					280					285					
Thr	Leu	Lys	Ile	Phe	Ile	Phe	Asn	Gln	Thr	Gly	Ile	Glu	Ala	Lys					
				290					295					300					
Lys	Asn	Val	Val	Val	Thr	Gln	Ala	Asp	Gln	Ile	Gly	Pro	Leu	Pro					
				305					310					315					
Ser	Thr	Leu	Ile	Lys	Ser	Val	Asp	Trp	Leu	Leu	Val	Phe	Ser	Leu					
				320					325					330					
Phe	Phe	Leu	Ile	Ser	Phe	Ile	Met	Tyr	Ala	Thr	Ile	Arg	Thr	Glu					
				335					340					345					
Ser	Ile	Arg	Trp	Leu	Ile	Pro	Gly	Gln	Glu	Gln	Glu	His	Val	Glu					
				350					355					360					

<210> 411
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 411
cacagagcca gaagtggcgg aatc 24

<210> 412
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 412
ccacatgttc ctgctcttgc cctgg 25

<210> 413
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 413
cggtagtgac tgtactctag tcctgtttta caccocgtgg tgccg 45

<210> 414
<211> 1196
<212> DNA
<213> Homo sapiens

<400> 414
cccggctccg ctccctctgc cccctcgggg tcgcgcgccc acgatgctgc 50
agggccctgg ctgcgtgctg ctgctcttcc tcgcctcgca ctgctgcctg 100
ggctcggcgc gcgggctctt cctctttggc cagcccgact tctcctacaa 150
gcgcagcaat tgcaagccca tcccggtcaa cctgcagctg tgccacggca 200
tcgaatacca gaacatgcgg ctgcccacc tgctgggcca cgagaccatg 250
aaggaggtgc tggagcaggc cggcgcttgg atcccgctgg tcatgaagca 300
gtgccacccg gacaccaaga agttcctgtg ctgcgtcttc gccccgtct 350
gctcgatga cctagacgag accatccagc catgccactc gctctgcgtg 400
caggtgaagg accgctgcgc cccggtcatg tccgccttcg gcttcccctg 450
gcccagacatg cttgagtgcg accgtttccc ccaggacaac gacctttgca 500
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 ggaaacgctt tgtaaaaaatg attttgcact gaaaataaaaa gtgaaggaga 650
 taacctacat caaccgagat accaaaaatca tcctggagac caagagcaag 700
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 ctcccgagc atccgcaagc tgcagtgcata gtcccgcat cctgatggct 950
 ccgacaggcc tgctccagag cacggctgac catttctgct ccgggatctc 1000
 agctcccgctt ccccaagcac actcctagct gctccagtct cagcctgggc 1050
 agcttcccc tgccttttgc acgtttgcat cccagcatt tcctgagtta 1100
 taaggccaca ggagtggata gctgttttca cctaaaggaa aagcccaccc 1150
 gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415
 <211> 295
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser
 1 5 10 15
 His Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln
 20 25 30
 Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val
 35 40 45
 Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu
 50 55 60
 Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln
 65 70 75
 Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp
 80 85 90
 Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp
 95 100 105
 Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln
 110 115 120
 Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro
 125 130 135

Trp	Pro	Asp	Met	Leu	Glu	Cys	Asp	Arg	Phe	Pro	Gln	Asp	Asn	Asp	
				140					145					150	
Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala	Thr	
				155					160					165	
Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	Asn	Lys	Asn	Asp	
				170					175					180	
Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	Asp	Phe	Ala	
				185					190					195	
Leu	Lys	Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	Asp	Thr	
				200					205					210	
Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	
				215					220					225	
Gly	Val	Ser	Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	
				230					235					240	
Asp	Ser	Leu	Gln	Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	
				245					250					255	
Pro	Tyr	Leu	Val	Met	Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	
				260					265					270	
Thr	Ser	Val	Lys	Arg	Trp	Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	
				275					280					285	
Ile	Ser	Arg	Ser	Ile	Arg	Lys	Leu	Gln	Cys						
				290					295						

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 416
 cctggctcgc tgctgctgct c 21

<210> 417
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 417
 cctcacaggt gcactgcaag ctgtc 25

<210> 418
 <211> 47
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

ctcttcctct ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

gtggaggccg ccgacgatgg cggggccgac ggaggccgag acgggggttg 50

ccgagccccg ggccctgtgc gcgcagcggg gccaccgcac ctacgcgcgc 100

cgctgggtgt tcctgtctgc gatcagcctg ctcaactgct ccaacgccac 150

gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200

tcctgtccat ggagcagatc aactggctgt cactggctta cctcgtggta 250

tccaccccat ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300

ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350

tacgcatggt gccctgcatg gttgttggga cccaaaaccc atttgccttc 400

ctcatgggtg gccagagcct ctgtgccctt gccagagcc tggatcatctt 450

ctctccagcc aagctggctg ccttgtgggt cccagagcac cagcgagcca 500

cggccaacat gctcgcacc atgtcgaacc ctctgggcgt ccttgtggcc 550

aatgtgctgt cccctgtgct ggtcaagaag ggtgaggaca ttccgttaat 600

gctcgggtgc tataccatcc ctgctggcgt cgtctgcctg ctgtccacca 650

tctgcctgtg ggagagtgtg cccccaccc cgccctctgc cggggctgcc 700

agctccacct cagagaagtt cctggatggg ctcaagctgc agctcatgtg 750

gaacaaggcc tatgtcatcc tggctgtgtg cttgggggga atgatcggga 800

tctctgccag cttctcagcc ctctggagc agatcctctg tgcaagcggc 850

cactccagtg ggttttccgg cctctgtggc gctctcttca tcacgtttgg 900

gatcctgggg gcactggctc tcggccccta tgtggaccgg accaagcact 950

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cacctgctcg ctgctcgggc tgtttggctt ctcggtgggc cccgtggcca 1100

tggagttggc ggtcgagtgt tccttccccg tgggggaggg ggctgccaca 1150
 ggcatgatct ttgtgctggg gcaggccgag ggaataactca tcatgctggc 1200
 aatgacggca ctgactgtgc gacgctcgga gccgtccttg tccacctgcc 1250
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 ccgtgggcgg cgcagactca gggccgggtg tggaccgagg gggagcagga 1450
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 cccggctggg tctcactcct ccttctcctc cccgtgggtg atcacgtagc 1700
 tgagcgcctt gtagtccagg ttgcccgcca catcgatgga ggcgaaactgg 1750
 aacatctggt ccacctgcgg gcgggggcga aagggtcctt tgcgggctcc 1800
 gggagcgaat tacaagcgcg cacctgaaaa 1830

<210> 420
 <211> 560
 <212> PRT
 <213> Homo sapiens

<400> 420
 Met Ala Gly Pro Thr Glu Ala Glu Thr Gly Leu Ala Glu Pro Arg
 1 5 10 15
 Ala Leu Cys Ala Gln Arg Gly His Arg Thr Tyr Ala Arg Arg Trp
 20 25 30
 Val Phe Leu Leu Ala Ile Ser Leu Leu Asn Cys Ser Asn Ala Thr
 35 40 45
 Leu Trp Leu Ser Phe Ala Pro Val Ala Asp Val Ile Ala Glu Asp
 50 55 60
 Leu Val Leu Ser Met Glu Gln Ile Asn Trp Leu Ser Leu Val Tyr
 65 70 75
 Leu Val Val Ser Thr Pro Phe Gly Val Ala Ala Ile Trp Ile Leu
 80 85 90
 Asp Ser Val Gly Leu Arg Ala Ala Thr Ile Leu Gly Ala Trp Leu
 95 100 105
 Asn Phe Ala Gly Ser Val Leu Arg Met Val Pro Cys Met Val Val

	110		115		120
Gly Thr Gln Asn	Pro Phe Ala Phe Leu	Met Gly Gly Gln Ser	Leu		
	125	130	135		
Cys Ala Leu Ala	Gln Ser Leu Val Ile	Phe Ser Pro Ala Lys	Leu		
	140	145	150		
Ala Ala Leu Trp	Phe Pro Glu His Gln	Arg Ala Thr Ala Asn	Met		
	155	160	165		
Leu Ala Thr Met	Ser Asn Pro Leu Gly	Val Leu Val Ala Asn	Val		
	170	175	180		
Leu Ser Pro Val	Leu Val Lys Lys Gly	Glu Asp Ile Pro Leu	Met		
	185	190	195		
Leu Gly Val Tyr	Thr Ile Pro Ala Gly	Val Val Cys Leu Leu	Ser		
	200	205	210		
Thr Ile Cys Leu	Trp Glu Ser Val Pro	Pro Thr Pro Pro Ser	Ala		
	215	220	225		
Gly Ala Ala Ser	Ser Thr Ser Glu Lys	Phe Leu Asp Gly Leu	Lys		
	230	235	240		
Leu Gln Leu Met	Trp Asn Lys Ala Tyr	Val Ile Leu Ala Val	Cys		
	245	250	255		
Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala Leu	Leu		
	260	265	270		
Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser	Gly		
	275	280	285		
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly Ala	Leu		
	290	295	300		
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu	Ala		
	305	310	315		
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro	Phe		
	320	325	330		
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala	Ala		
	335	340	345		
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro	Val		
	350	355	360		
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu	Gly		
	365	370	375		
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly	Ile		
	380	385	390		
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser	Glu		
	395	400	405		

Pro	Ser	Leu	Ser	Thr	Cys	Gln	Gln	Gly	Glu	Asp	Pro	Leu	Asp	Trp
				410					415					420
Thr	Val	Ser	Leu	Leu	Leu	Met	Ala	Gly	Leu	Cys	Thr	Phe	Phe	Ser
				425					430					435
Cys	Ile	Leu	Ala	Val	Phe	Phe	His	Thr	Pro	Tyr	Arg	Arg	Leu	Gln
				440					445					450
Ala	Glu	Ser	Gly	Glu	Pro	Pro	Ser	Thr	Arg	Asn	Ala	Val	Gly	Gly
				455					460					465
Ala	Asp	Ser	Gly	Pro	Gly	Val	Asp	Arg	Gly	Gly	Ala	Gly	Arg	Ala
				470					475					480
Gly	Val	Leu	Gly	Pro	Ser	Thr	Ala	Thr	Pro	Glu	Cys	Thr	Ala	Arg
				485					490					495
Gly	Ala	Ser	Leu	Glu	Asp	Pro	Arg	Gly	Pro	Gly	Ser	Pro	His	Pro
				500					505					510
Ala	Cys	His	Arg	Ala	Thr	Pro	Arg	Ala	Gln	Gly	Pro	Ala	Ala	Thr
				515					520					525
Asp	Ala	Pro	Ser	Arg	Pro	Gly	Arg	Leu	Ala	Gly	Arg	Val	Gln	Ala
				530					535					540
Ser	Arg	Phe	Ile	Asp	Pro	Ala	Gly	Ser	His	Ser	Ser	Phe	Ser	Ser
				545					550					555
Pro	Trp	Val	Ile	Thr										
				560										

<210> 421
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 421
 agcttctcag ccctcctgga gcag 24

<210> 422
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 422
 cgggtcaata aacctggacg cttgg 25

<210> 423
 <211> 43
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcaactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

gtcccacatc ctgctcaact gggtcaggtc cctcttagac cagctcttgt 50
ccatcatittg ctgaagtggc ccaactagtt cccagtagg gggctctccc 100
tggcaattct tgatcggcgt ttggacatct cagatcgctt ccaatgaaga 150
tggccttgcc ttggggtcct gcttgtttca taatcatcta actatgggac 200
aaggttgtgc cggcagctct gggggaagga gcacggggct gatcaagcca 250
tccaggaaac actggaggac ttgtccagcc ttgaaagaac tctagtgggt 300
tctgaatcta gccacttgg cggttaagcat gatgcaactt ctgcaacttc 350
tgctggggct tttggggcca ggtggctact tatttctttt aggggattgt 400
caggagggtga ccactctcac ggtgaaatac caagtgtcag aggaagtgcc 450
atctggtaca gtgatcggga agctgtccca ggaactgggc cgggaggaga 500
ggcggaggca agctggggcc gccttcagcgt tggtgcagct gcctcaggcg 550
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gagctcttga cccagacaca ggccctaaca ccctgcacac ctacactctg 850
tctcccagtg agcactttgc cttggatgtc attgtgggccc ctgatgagac 900
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ccctgcgttt gctgagagtt cactggcact ggaaatccaa gaagatgctg 1100

cacctggtac gcttctcata aaactgaccg ccacagaccc tgaccaaggc 1150
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 aaatataccc tcaactctgtt agcccaagac caaggactcc agcccttacc 1650
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 gagggtcatg tttgtcacca gtgtggacca cctgagggac tcagcccga 2450
 agcctggggc cttgagcatg tcgatgctga cggatgatctg cctggctgta 2500
 ctgttgggca tcttcgggtt gatcctggct ttgttcatgt ccatctgccg 2550

gacagaaaag aaggacaaca gggcctacaa ctgtcgggag gccgagtcca 2600
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 gctgcaagac acggtcaacc tccttttcaa ccatcccagg cagaggaatg 2900
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 cagcacaggt ctggccctgg accggctgag cggccctgac ccggcctgga 3500
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 ctggatccaa gaaccagggg cctgaggatc tgtggacaag agctgggttc 3950
 taaaatcttg taactcacta gctagcggcg gcctgagaac tttaggggtga 4000

ctgatgctac cccacagag gaggcaagag cccaggact aacagctgac 4050
 tgaccaaagc agccccttgt aagcagctct gagtcttttg gaggacaggg 4100
 acggtttgtg gctgagataa gtgtttcctg gcaaacata tgtggagcac 4150
 aaagggtcag tcctctggca gaacagatgc cacggagtat cacaggcagg 4200
 aaaggggtggc cttcttgggt agcaggagtc agggggctgt accctggggg 4250
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 aaaaaaaaaa aaa 4313

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 <211> 1184
 <212> PRT
 <213> Homo sapiens

<400> 425
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 Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val
 35 40 45
 Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg
 50 55 60
 Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu
 65 70 75
 Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg
 80 85 90
 Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu
 95 100 105
 Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His
 110 115 120
 Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe
 125 130 135
 Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu
 140 145 150
 Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly
 155 160 165
 Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe
 170 175 180
 Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu
 185 190 195

Leu Ile Val Val	Lys Glu Leu Asp Arg	Glu Ile His Ser Phe	Phe
	200	205	210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn	Gly Asn Pro Pro Lys	Ser
	215	220	225
Gly Thr Ser Leu	Val Lys Val Asn Val	Leu Asp Ser Asn Asp	Asn
	230	235	240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu	Ala Leu Glu Ile Gln	Glu
	245	250	255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile	Lys Leu Thr Ala Thr	Asp
	260	265	270
Pro Asp Gln Gly	Pro Asn Gly Glu Val	Glu Phe Phe Leu Ser	Lys
	275	280	285
His Met Pro Pro	Glu Val Leu Asp Thr	Phe Ser Ile Asp Ala	Lys
	290	295	300
Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys	Asn
	305	310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly Pro	Asn
	320	325	330
Pro Ile Pro Ala	His Cys Lys Val Leu	Ile Lys Val Leu Asp	Val
	335	340	345
Asn Asp Asn Ile	Pro Ser Ile His Val	Thr Trp Ala Ser Gln	Pro
	350	355	360
Ser Leu Val Ser	Glu Ala Leu Pro Lys	Asp Ser Phe Ile Ala	Leu
	365	370	375
Val Met Ala Asp	Asp Leu Asp Ser Gly	His Asn Gly Leu Val	His
	380	385	390
Cys Trp Leu Ser	Gln Glu Leu Gly His	Phe Arg Leu Lys Arg	Thr
	395	400	405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr	Asn Ala Thr Leu Asp	Arg
	410	415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr	Leu Leu Ala Gln Asp	Gln
	425	430	435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys	Gln Leu Ser Ile Gln	Ile
	440	445	450
Ser Asp Ile Asn	Asp Asn Ala Pro Val	Phe Glu Lys Ser Arg	Tyr
	455	460	465
Glu Val Ser Thr	Arg Glu Asn Asn Leu	Pro Ser Leu His Leu	Ile
	470	475	480
Thr Ile Lys Ala	His Asp Ala Asp Leu	Gly Ile Asn Gly Lys	Val

09978187 101501

485					490					495				
Ser	Tyr	Arg	Ile	Gln	Asp	Ser	Pro	Val	Ala	His	Leu	Val	Ala	Ile
				500					505					510
Asp	Ser	Asn	Thr	Gly	Glu	Val	Thr	Ala	Gln	Arg	Ser	Leu	Asn	Tyr
				515					520					525
Glu	Glu	Met	Ala	Gly	Phe	Glu	Phe	Gln	Val	Ile	Ala	Glu	Asp	Ser
				530					535					540
Gly	Gln	Pro	Met	Leu	Ala	Ser	Ser	Val	Ser	Val	Trp	Val	Ser	Leu
				545					550					555
Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	Glu	Val	Val	Gln	Pro	Val	Leu
				560					565					570
Ser	Asp	Gly	Lys	Ala	Ser	Leu	Ser	Val	Leu	Val	Asn	Ala	Ser	Thr
				575					580					585
Gly	His	Leu	Leu	Val	Pro	Ile	Glu	Thr	Pro	Asn	Gly	Leu	Gly	Pro
				590					595					600
Ala	Gly	Thr	Asp	Thr	Pro	Pro	Leu	Ala	Thr	His	Ser	Ser	Arg	Pro
				605					610					615
Phe	Leu	Leu	Thr	Thr	Ile	Val	Ala	Arg	Asp	Ala	Asp	Ser	Gly	Ala
				620					625					630
Asn	Gly	Glu	Pro	Leu	Tyr	Ser	Ile	Arg	Asn	Gly	Asn	Glu	Ala	His
				635					640					645
Leu	Phe	Ile	Leu	Asn	Pro	His	Thr	Gly	Gln	Leu	Phe	Val	Asn	Val
				650					655					660
Thr	Asn	Ala	Ser	Ser	Leu	Ile	Gly	Ser	Glu	Trp	Glu	Leu	Glu	Ile
				665					670					675
Val	Val	Glu	Asp	Gln	Gly	Ser	Pro	Pro	Leu	Gln	Thr	Arg	Ala	Leu
				680					685					690
Leu	Arg	Val	Met	Phe	Val	Thr	Ser	Val	Asp	His	Leu	Arg	Asp	Ser
				695					700					705
Ala	Arg	Lys	Pro	Gly	Ala	Leu	Ser	Met	Ser	Met	Leu	Thr	Val	Ile
				710					715					720
Cys	Leu	Ala	Val	Leu	Leu	Gly	Ile	Phe	Gly	Leu	Ile	Leu	Ala	Leu
				725					730					735
Phe	Met	Ser	Ile	Cys	Arg	Thr	Glu	Lys	Lys	Asp	Asn	Arg	Ala	Tyr
				740					745					750
Asn	Cys	Arg	Glu	Ala	Glu	Ser	Thr	Tyr	Arg	Gln	Gln	Pro	Lys	Arg
				755					760					765
Pro	Gln	Lys	His	Ile	Gln	Lys	Ala	Asp	Ile	His	Leu	Val	Pro	Val
				770					775					780

Leu	Arg	Gly	Gln	Ala	Gly	Glu	Pro	Cys	Glu	Val	Gly	Gln	Ser	His	
				785					790					795	
Lys	Asp	Val	Asp	Lys	Glu	Ala	Met	Met	Glu	Ala	Gly	Trp	Asp	Pro	
				800					805					810	
Cys	Leu	Gln	Ala	Pro	Phe	His	Leu	Thr	Pro	Thr	Leu	Tyr	Arg	Thr	
				815					820					825	
Leu	Arg	Asn	Gln	Gly	Asn	Gln	Gly	Ala	Pro	Ala	Glu	Ser	Arg	Glu	
				830					835					840	
Val	Leu	Gln	Asp	Thr	Val	Asn	Leu	Leu	Phe	Asn	His	Pro	Arg	Gln	
				845					850					855	
Arg	Asn	Ala	Ser	Arg	Glu	Asn	Leu	Asn	Leu	Pro	Glu	Pro	Gln	Pro	
				860					865					870	
Ala	Thr	Gly	Gln	Pro	Arg	Ser	Arg	Pro	Leu	Lys	Val	Ala	Gly	Ser	
				875					880					885	
Pro	Thr	Gly	Arg	Leu	Ala	Gly	Asp	Gln	Gly	Ser	Glu	Glu	Ala	Pro	
				890					895					900	
Gln	Arg	Pro	Pro	Ala	Ser	Ser	Ala	Thr	Leu	Arg	Arg	Gln	Arg	His	
				905					910					915	
Leu	Asn	Gly	Lys	Val	Ser	Pro	Glu	Lys	Glu	Ser	Gly	Pro	Arg	Gln	
				920					925					930	
Ile	Leu	Arg	Ser	Leu	Val	Arg	Leu	Ser	Val	Ala	Ala	Phe	Ala	Glu	
				935					940					945	
Arg	Asn	Pro	Val	Glu	Glu	Leu	Thr	Val	Asp	Ser	Pro	Pro	Val	Gln	
				950					955					960	
Gln	Ile	Ser	Gln	Leu	Leu	Ser	Leu	Leu	His	Gln	Gly	Gln	Phe	Gln	
				965					970					975	
Pro	Lys	Pro	Asn	His	Arg	Gly	Asn	Lys	Tyr	Leu	Ala	Lys	Pro	Gly	
				980					985					990	
Gly	Ser	Arg	Ser	Ala	Ile	Pro	Asp	Thr	Asp	Gly	Pro	Ser	Ala	Arg	
				995					1000					1005	
Ala	Gly	Gly	Gln	Thr	Asp	Pro	Glu	Gln	Glu	Glu	Gly	Pro	Leu	Asp	
				1010					1015					1020	
Pro	Glu	Glu	Asp	Leu	Ser	Val	Lys	Gln	Leu	Leu	Glu	Glu	Glu	Leu	
				1025					1030					1035	
Ser	Ser	Leu	Leu	Asp	Pro	Ser	Thr	Gly	Leu	Ala	Leu	Asp	Arg	Leu	
				1040					1045					1050	
Ser	Ala	Pro	Asp	Pro	Ala	Trp	Met	Ala	Arg	Leu	Ser	Leu	Pro	Leu	
				1055					1060					1065	
Thr	Thr	Asn	Tyr	Arg	Asp	Asn	Val	Ile	Ser	Pro	Asp	Ala	Ala	Ala	

1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala		
1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val		
1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser		
1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser		
1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala		
1145	1150	1155
Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr		
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Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu		
1175	1180	

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 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 427
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 427
 gtgacgtgga tgcttgggat gttg 24

<210> 428
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 428
 tggacacctt cagtattgat gccaaagacag gccaggtcat tctgcgtcga 50

<210> 429
 <211> 2037

<212> DNA
<213> Homo sapiens

<400> 429

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ggcctcgggg agtgggaagt ggaggcagga gccttcctta cacttcgcca 150
tgagtttcct catcgactcc agcatcatga ttacctcca gatactattt 200
tttggatttg ggtggctttt cttcatgcgc caattgttta aagactatga 250
gatacgtcag tatgttgtac aggtgatctt ctccgtgacg tttgcatttt 300
cttgaccat gtttgagctc atcatctttg aaatcttagg agtattgaat 350
agcagctccc gttattttca ctggaaaatg aacctgtgtg taattctgct 400
gatcctgggtt ttcattggtgc ctttttacat tggctatttt attgtgagca 450
atatccgact actgcataaa caacgactgc ttttttcctg tctcttatgg 500
ctgaccttta tgtatttctt ctggaaacta ggagatccct tccccattct 550
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ggatattcta gccctggaac ggcgactgct gcaaaccatg gatatgatca 750
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 gtgaaaaata cactggaact ctggggcaag acatgtctat ggtagctgag 1850
 ccaaacacgt aggatttccg ttttaagggt cacatggaaa aggttatagc 1900
 tttgccttga gattgactca ttaaaatcag agactgtaac aaaaaaaaaa 1950
 aaaaaaaaaa agggcgccgc cgactctaga gtcgacctgc agaagcttgg 2000
 ccgccatggc ccaacttggt tattgcagct tataatg 2037

<210> 430
 <211> 455
 <212> PRT
 <213> Homo sapiens

<400> 430
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 Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser
 35 40 45
 Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe
 50 55 60
 Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp
 65 70 75
 Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val
 80 85 90
 Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu
 95 100 105
 His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe
 110 115 120

Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser	125	130	135
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val	140	145	150
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly	155	160	165
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn	170	175	180
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln	185	190	195
Thr	Met	Asp	Met	Ile	Ile	Ser	Lys	Lys	Lys	Arg	Met	Ala	Met	Ala	200	205	210
Arg	Arg	Thr	Met	Phe	Gln	Lys	Gly	Glu	Val	His	Asn	Lys	Pro	Ser	215	220	225
Gly	Phe	Trp	Gly	Met	Ile	Lys	Ser	Val	Thr	Thr	Ser	Ala	Ser	Gly	230	235	240
Ser	Glu	Asn	Leu	Thr	Leu	Ile	Gln	Gln	Glu	Val	Asp	Ala	Leu	Glu	245	250	255
Glu	Leu	Ser	Arg	Gln	Leu	Phe	Leu	Glu	Thr	Ala	Asp	Leu	Tyr	Ala	260	265	270
Thr	Lys	Glu	Arg	Ile	Glu	Tyr	Ser	Lys	Thr	Phe	Lys	Gly	Lys	Tyr	275	280	285
Phe	Asn	Phe	Leu	Gly	Tyr	Phe	Phe	Ser	Ile	Tyr	Cys	Val	Trp	Lys	290	295	300
Ile	Phe	Met	Ala	Thr	Ile	Asn	Ile	Val	Phe	Asp	Arg	Val	Gly	Lys	305	310	315
Thr	Asp	Pro	Val	Thr	Arg	Gly	Ile	Glu	Ile	Thr	Val	Asn	Tyr	Leu	320	325	330
Gly	Ile	Gln	Phe	Asp	Val	Lys	Phe	Trp	Ser	Gln	His	Ile	Ser	Phe	335	340	345
Ile	Leu	Val	Gly	Ile	Ile	Ile	Val	Thr	Ser	Ile	Arg	Gly	Leu	Leu	350	355	360
Ile	Thr	Leu	Thr	Lys	Phe	Phe	Tyr	Ala	Ile	Ser	Ser	Ser	Lys	Ser	365	370	375
Ser	Asn	Val	Ile	Val	Leu	Leu	Leu	Ala	Gln	Ile	Met	Gly	Met	Tyr	380	385	390
Phe	Val	Ser	Ser	Val	Leu	Leu	Ile	Arg	Met	Ser	Met	Pro	Leu	Glu	395	400	405
Tyr	Arg	Thr	Ile	Ile	Thr	Glu	Val	Leu	Gly	Glu	Leu	Gln	Phe	Asn			

410	415	420
Phe Tyr His Arg Trp Phe Asp Val Ile	Phe Leu Val Ser Ala Leu	
425	430	435
Ser Ser Ile Leu Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro Glu	
440	445	450
Lys Gln Met Ala Pro		
455		

<210> 431
 <211> 407
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 78, 81, 113, 157, 224, 297
 <223> unknown base

<400> 431
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 tcgactccag catcatgatt acctcccnga nactattttt tggatttggg 100
 tggcttttct tcngcgccaa tgtttaaaga ctatgagata cgtcagtatg 150
 ttgtacnggt gatcttctcc gtgacgtttg ccatttcttg caccatgttt 200
 gagctcatca tctttgaaat ctinggagta ttgaatagca gctcccgtta 250
 ttttacttgg aaaatgaacc tgtgtgtaat tctgctgatc ctggttntca 300
 tggtgccitt ttacattggc tattttattg tgagcaatat ccgactactg 350
 cataaacaac gactgctttt ttctgtcttc ttatggctga cctttatgta 400
 tttccag 407

<210> 432
 <211> 457
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
 <223> unknown base

<400> 432
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 gccaaagggt tctttnttga attccgggtt nngnatacct tcccagaaaa 100
 tatttttttg atttggggta gntttttttc atgcgccaat tgtttaaaga 150
 ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgtttg 200

cattttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250
 ttgaatagca gctcccgta ttttcaactgg aaaatgaacc tgtgtgtaat 300
 tctgctgatc ctggttttca tgggtgccttt ttacattggc tattttattg 350
 tgagcaatat ccgactactg cataaacaac gactgctttt ttccctgtctn 400
 ttatggctga cctttatgta tttnttntgg aaantaggag atccctttcc 450
 cattctc 457

<210> 433
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 433
 aagtggagcc ggagccttcc 20

<210> 434
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 434
 tcgtgttta tgcagtagtc gg 22

<210> 435
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 435
 attgtttaaa gactatgaga tacgtcagta tgttgtagag g 41

<210> 436
 <211> 3951
 <212> DNA
 <213> Homo sapiens

<400> 436
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 gggcctccgg gatttgctac ctttttggct ccctgctcgt cgaactgctc 100
 ttctcacggg ctgtcgcctt caatctggac gtgatgggtg ccttgcgcaa 150
 ggagggcgag ccaggcagcc tcttcggctt ctctgtggcc ctgcaccggc 200

agttgcagcc ccgaccccag agctggctgc tggagggtgc tccccaggcc 250
 ctggctcttc ctgggcagca ggcgaatcgc actggaggcc tcttcgcttg 300
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 gccatgttcc agctccagga aaatgtcaaa gacaagcttc gggccattgt 1800
 agtgaccttg tcctacagtc tccagacccc tcggctccgg cgacaggctc 1850
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<211> 1141
<212> PRT
<213> Homo sapiens

<400> 437

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Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
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Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
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Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
				65					70					75
Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly

09978187 101501

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Val	Asp	Ile	Asp	Gln	Gly	Ala	Asp	Met	Gln	Lys	Glu	Ser	Lys	Glu
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Asn	Gln	Trp	Leu	Gly	Val	Ser	Val	Arg	Ser	Gln	Gly	Pro	Gly	Gly
				125					130					135
Lys	Ile	Val	Thr	Cys	Ala	His	Arg	Tyr	Glu	Ala	Arg	Gln	Arg	Val
				140					145					150
Asp	Gln	Ile	Leu	Glu	Thr	Arg	Asp	Met	Ile	Gly	Arg	Cys	Phe	Val
				155					160					165
Leu	Ser	Gln	Asp	Leu	Ala	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Gly	Glu
				170					175					180
Trp	Lys	Phe	Cys	Glu	Gly	Arg	Pro	Gln	Gly	His	Glu	Gln	Phe	Gly
				185					190					195
Phe	Cys	Gln	Gln	Gly	Thr	Ala	Ala	Ala	Phe	Ser	Pro	Asp	Ser	His
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Tyr	Leu	Leu	Phe	Gly	Ala	Pro	Gly	Thr	Tyr	Asn	Trp	Lys	Gly	Thr
				215					220					225
Ala	Arg	Val	Glu	Leu	Cys	Ala	Gln	Gly	Ser	Ala	Asp	Leu	Ala	His
				230					235					240
Leu	Asp	Asp	Gly	Pro	Tyr	Glu	Ala	Gly	Gly	Glu	Lys	Glu	Gln	Asp
				245					250					255
Pro	Arg	Leu	Ile	Pro	Val	Pro	Ala	Asn	Ser	Tyr	Phe	Gly	Phe	Ser
				260					265					270
Ile	Asp	Ser	Gly	Lys	Gly	Leu	Val	Arg	Ala	Glu	Glu	Leu	Ser	Phe
				275					280					285
Val	Ala	Gly	Ala	Pro	Arg	Ala	Asn	His	Lys	Gly	Ala	Val	Val	Ile
				290					295					300
Leu	Arg	Lys	Asp	Ser	Ala	Ser	Arg	Leu	Val	Pro	Glu	Val	Met	Leu
				305					310					315
Ser	Gly	Glu	Arg	Leu	Thr	Ser	Gly	Phe	Gly	Tyr	Ser	Leu	Ala	Val
				320					325					330
Ala	Asp	Leu	Asn	Ser	Asp	Gly	Trp	Pro	Asp	Leu	Ile	Val	Gly	Ala
				335					340					345
Pro	Tyr	Phe	Phe	Glu	Arg	Gln	Glu	Glu	Leu	Gly	Gly	Ala	Val	Tyr
				350					355					360
Val	Tyr	Leu	Asn	Gln	Gly	Gly	His	Trp	Ala	Gly	Ile	Ser	Pro	Leu
				365					370					375

Arg	Leu	Cys	Gly	Ser	Pro	Asp	Ser	Met	Phe	Gly	Ile	Ser	Leu	Ala
				380					385					390
Val	Leu	Gly	Asp	Leu	Asn	Gln	Asp	Gly	Phe	Pro	Asp	Ile	Ala	Val
				395					400					405
Gly	Ala	Pro	Phe	Asp	Gly	Asp	Gly	Lys	Val	Phe	Ile	Tyr	His	Gly
				410					415					420
Ser	Ser	Leu	Gly	Val	Val	Ala	Lys	Pro	Ser	Gln	Val	Leu	Glu	Gly
				425					430					435
Glu	Ala	Val	Gly	Ile	Lys	Ser	Phe	Gly	Tyr	Ser	Leu	Ser	Gly	Ser
				440					445					450
Leu	Asp	Met	Asp	Gly	Asn	Gln	Tyr	Pro	Asp	Leu	Leu	Val	Gly	Ser
				455					460					465
Leu	Ala	Asp	Thr	Ala	Val	Leu	Phe	Arg	Ala	Arg	Pro	Ile	Leu	His
				470					475					480
Val	Ser	His	Glu	Val	Ser	Ile	Ala	Pro	Arg	Ser	Ile	Asp	Leu	Glu
				485					490					495
Gln	Pro	Asn	Cys	Ala	Gly	Gly	His	Ser	Val	Cys	Val	Asp	Leu	Arg
				500					505					510
Val	Cys	Phe	Ser	Tyr	Ile	Ala	Val	Pro	Ser	Ser	Tyr	Ser	Pro	Thr
				515					520					525
Val	Ala	Leu	Asp	Tyr	Val	Leu	Asp	Ala	Asp	Thr	Asp	Arg	Arg	Leu
				530					535					540
Arg	Gly	Gln	Val	Pro	Arg	Val	Thr	Phe	Leu	Ser	Arg	Asn	Leu	Glu
				545					550					555
Glu	Pro	Lys	His	Gln	Ala	Ser	Gly	Thr	Val	Trp	Leu	Lys	His	Gln
				560					565					570
His	Asp	Arg	Val	Cys	Gly	Asp	Ala	Met	Phe	Gln	Leu	Gln	Glu	Asn
				575					580					585
Val	Lys	Asp	Lys	Leu	Arg	Ala	Ile	Val	Val	Thr	Leu	Ser	Tyr	Ser
				590					595					600
Leu	Gln	Thr	Pro	Arg	Leu	Arg	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
				605					610					615
Pro	Pro	Val	Ala	Pro	Ile	Leu	Asn	Ala	His	Gln	Pro	Ser	Thr	Gln
				620					625					630
Arg	Ala	Glu	Ile	His	Phe	Leu	Lys	Gln	Gly	Cys	Gly	Glu	Asp	Lys
				635					640					645
Ile	Cys	Gln	Ser	Asn	Leu	Gln	Leu	Val	His	Ala	Arg	Phe	Cys	Thr
				650					655					660
Arg	Val	Ser	Asp	Thr	Glu	Phe	Gln	Pro	Leu	Pro	Met	Asp	Val	Asp

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Gly	Thr	Thr	Ala	Leu	Phe	Ala	Leu	Ser		Gly	Gln	Pro	Val	Ile	Gly				
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				695					700					705					
Gln	Ala	Asp	Gly	Asp	Asp	Ala	His	Glu	Ala	Gln	Leu	Leu	Val	Met					
				710					715					720					
Leu	Pro	Asp	Ser	Leu	His	Tyr	Ser	Gly	Val	Arg	Ala	Leu	Asp	Pro					
				725					730					735					
Ala	Glu	Lys	Pro	Leu	Cys	Leu	Ser	Asn	Glu	Asn	Ala	Ser	His	Val					
				740					745					750					
Glu	Cys	Glu	Leu	Gly	Asn	Pro	Met	Lys	Arg	Gly	Ala	Gln	Val	Thr					
				755					760					765					
Phe	Tyr	Leu	Ile	Leu	Ser	Thr	Ser	Gly	Ile	Ser	Ile	Glu	Thr	Thr					
				770					775					780					
Glu	Leu	Glu	Val	Glu	Leu	Leu	Leu	Ala	Thr	Ile	Ser	Glu	Gln	Glu					
				785					790					795					
Leu	His	Pro	Val	Ser	Ala	Arg	Ala	Arg	Val	Phe	Ile	Glu	Leu	Pro					
				800					805					810					
Leu	Ser	Ile	Ala	Gly	Met	Ala	Ile	Pro	Gln	Gln	Leu	Phe	Phe	Ser					
				815					820					825					
Gly	Val	Val	Arg	Gly	Glu	Arg	Ala	Met	Gln	Ser	Glu	Arg	Asp	Val					
				830					835					840					
Gly	Ser	Lys	Val	Lys	Tyr	Glu	Val	Thr	Val	Ser	Asn	Gln	Gly	Gln					
				845					850					855					
Ser	Leu	Arg	Thr	Leu	Gly	Ser	Ala	Phe	Leu	Asn	Ile	Met	Trp	Pro					
				860					865					870					
His	Glu	Ile	Ala	Asn	Gly	Lys	Trp	Leu	Leu	Tyr	Pro	Met	Gln	Val					
				875					880					885					
Glu	Leu	Glu	Gly	Gly	Gln	Gly	Pro	Gly	Gln	Lys	Gly	Leu	Cys	Ser					
				890					895					900					
Pro	Arg	Pro	Asn	Ile	Leu	His	Leu	Asp	Val	Asp	Ser	Arg	Asp	Arg					
				905					910					915					
Arg	Arg	Arg	Glu	Leu	Glu	Pro	Pro	Glu	Gln	Gln	Glu	Pro	Gly	Glu					
				920					925					930					
Arg	Gln	Glu	Pro	Ser	Met	Ser	Trp	Trp	Pro	Val	Ser	Ser	Ala	Glu					
				935					940					945					
Lys	Lys	Lys	Asn	Ile	Thr	Leu	Asp	Cys	Ala	Arg	Gly	Thr	Ala	Asn					
				950					955					960					

Cys	Val	Val	Phe	Ser	Cys	Pro	Leu	Tyr	Ser	Phe	Asp	Arg	Ala	Ala	
				965					970					975	
Val	Leu	His	Val	Trp	Gly	Arg	Leu	Trp	Asn	Ser	Thr	Phe	Leu	Glu	
				980					985					990	
Glu	Tyr	Ser	Ala	Val	Lys	Ser	Leu	Glu	Val	Ile	Val	Arg	Ala	Asn	
				995					1000					1005	
Ile	Thr	Val	Lys	Ser	Ser	Ile	Lys	Asn	Leu	Met	Leu	Arg	Asp	Ala	
				1010					1015					1020	
Ser	Thr	Val	Ile	Pro	Val	Met	Val	Tyr	Leu	Asp	Pro	Met	Ala	Val	
				1025					1030					1035	
Val	Ala	Glu	Gly	Val	Pro	Trp	Trp	Val	Ile	Leu	Leu	Ala	Val	Leu	
				1040					1045					1050	
Ala	Gly	Leu	Leu	Val	Leu	Ala	Leu	Leu	Val	Leu	Leu	Leu	Trp	Lys	
				1055					1060					1065	
Met	Gly	Phe	Phe	Lys	Arg	Ala	Lys	His	Pro	Glu	Ala	Thr	Val	Pro	
				1070					1075					1080	
Gln	Tyr	His	Ala	Val	Lys	Ile	Pro	Arg	Glu	Asp	Arg	Gln	Gln	Phe	
				1085					1090					1095	
Lys	Glu	Glu	Lys	Thr	Gly	Thr	Ile	Leu	Arg	Asn	Asn	Trp	Gly	Ser	
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Pro	Arg	Arg	Glu	Gly	Pro	Asp	Ala	His	Pro	Ile	Leu	Ala	Ala	Asp	
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<210> 438
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 439
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 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 439
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<210> 440
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 441
 <211> 1964
 <212> DNA
 <213> Homo sapiens

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 cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200
 ccgcggcggt ggctgcagcc ggggggcggg cggacggcgg taattttctg 250
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 aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtctta 1850
 aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900
 ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950
 aaaaaaaaaa aaaa 1964

<210> 442
 <211> 436
 <212> PRT
 <213> Homo sapiens

<400> 442
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 20 25 30
 Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu
 35 40 45
 Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys

50					55					60				
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro
				65					70					75
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys
				80					85					90
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp
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Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg
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Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile
				125					130					135
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val
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Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu
				155					160					165
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu
				170					175					180
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg
				185					190					195
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala
				200					205					210
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser
				215					220					225
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg
				230					235					240
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp
				245					250					255
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln
				260					265					270
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr
				275					280					285
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile
				290					295					300
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro
				305					310					315
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val
				320					325					330
Lys	Lys	Leu	Leu	Gly	Gln	Tyr	Ile	Pro	Leu	Cys	Asp	Glu	Asp	Gly
				335					340					345

Tyr	Tyr	Lys	Pro	Thr	Gln	Cys	His	Gly	Ser	Val	Gly	Gln	Cys	Trp
				350					355					360
Cys	Val	Asp	Arg	Tyr	Gly	Asn	Glu	Val	Met	Gly	Ser	Arg	Ile	Asn
				365					370					375
Gly	Val	Ala	Asp	Cys	Ala	Ile	Asp	Phe	Glu	Ile	Ser	Gly	Asp	Phe
				380					385					390
Ala	Ser	Gly	Asp	Phe	His	Glu	Trp	Thr	Asp	Asp	Glu	Asp	Asp	Glu
				395					400					405
Asp	Asp	Ile	Met	Asn	Asp	Glu	Asp	Glu	Ile	Glu	Asp	Asp	Asp	Glu
				410					415					420
Asp	Glu	Gly	Asp	Asp	Asp	Asp	Gly	Gly	Asp	Asp	His	Asp	Val	Tyr
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Ile

<210> 443
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 443
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<210> 444
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 444
 catcatggtc atcaccacca tcatcatc 28

<210> 445
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 445
 ggttactaca agccaacaca atgtcatggc agtggtggac agtgctgg 48

<210> 446
 <211> 3617
 <212> DNA
 <213> Homo sapiens

<400> 446
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gagcggagac aacagtacct gacgcctctt tcagcccggg atcgccccag 100
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gctctgcctc cgggtgctgt gcctggggcg gccggcttca caccttccct 200
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caaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850
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<210> 447
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 447
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 20 25 30
 Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys
 35 40 45
 Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile
 50 55 60
 Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His
 65 70 75
 Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys
 80 85 90
 Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met
 95 100 105
 Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile

	110		115		120
Phe Phe Glu Leu	Ile Leu Asp Asn Met	Gly Glu Gln Ala Gln	Glu		
	125		130		135
Gln Glu Asp Trp	Lys Lys Tyr Ile Thr	Gly Thr Asp Ile Leu	Asp		
	140		145		150
Met Lys Leu Glu	Asp Ile Leu Glu Ser	Ile Asn Ser Ile Lys	Ser		
	155		160		165
Arg Leu Ser Lys	Ser Gly His Ile Gln	Ile Leu Leu Arg Ala	Phe		
	170		175		180
Glu Ala Arg Asp	Arg Asn Ile Gln Glu	Ser Asn Phe Asp Arg	Val		
	185		190		195
Asn Phe Trp Ser	Met Val Asn Leu Val	Val Met Val Val Val	Ser		
	200		205		210
Ala Ile Gln Val	Tyr Met Leu Lys Ser	Leu Phe Glu Asp Lys	Arg		
	215		220		225
Lys Ser Arg Thr					

<210> 448
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 448
 cccagcaggg ctgggcgaca aga 23

<210> 449
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 449
 gtcttccagt ttcatatcca ata 23

<210> 450
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 450
 ccagaaggag cacggggaag ggcagccaga tcttgctgcc cat 43

<210> 451
 <211> 859
 <212> DNA
 <213> Homo sapiens

<400> 451
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 agcataccag atctcaccag agagtcgcag acactatgct gcctcccatg 100
 gccctgcca gtgtgtcctg gatgctgctt tctgcctca ttctcctgtg 150
 tcagggtcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200
 gctgtcccaa aggtccaag gcctatggct cccctgcta tgccttggtt 250
 ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300
 ctctggaaaa ctggtgtctg tgctcagtgg ggctgaggga tcttctgtgt 350
 cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400
 ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450
 gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500
 ccattctaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550
 ctgaagtgga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600
 gttcaaggac tagggcaggt ggaagtcag cagcctcagc ttggcgtgca 650
 gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700
 ttctcccaa actgccctac ctgactacct tgcatgatc ctcttctttt 750
 ttcttttttc ttacacttca ttacaggctt ttctctgtct tccatgtctt 800
 gagatctcag agaataataa taaaatggt actttataaa aaaaaaaaaa 850
 aaaaaaaaaa 859

<210> 452
 <211> 175
 <212> PRT
 <213> Homo sapiens

<400> 452
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 1 5 10 15
 Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln
 20 25 30
 Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys
 35 40 45
 Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser

	50		55		60
Trp Met Asp Ala Asp	Leu Ala Cys Gln Lys	Arg Pro Ser Gly Lys			
	65	70			75
Leu Val Ser Val Leu	Ser Gly Ala Glu Gly	Ser Phe Val Ser Ser			
	80	85			90
Leu Val Arg Ser Ile	Ser Asn Ser Tyr Ser	Tyr Ile Trp Ile Gly			
	95	100			105
Leu His Asp Pro Thr	Gln Gly Ser Glu Pro	Asp Gly Asp Gly Trp			
	110	115			120
Glu Trp Ser Ser Thr	Asp Val Met Asn Tyr	Phe Ala Trp Glu Lys			
	125	130			135
Asn Pro Ser Thr Ile	Leu Asn Pro Gly His	Cys Gly Ser Leu Ser			
	140	145			150
Arg Ser Thr Gly Phe	Leu Lys Trp Lys Asp	Tyr Asn Cys Asp Ala			
	155	160			165
Lys Leu Pro Tyr Val	Cys Lys Phe Lys Asp				
	170	175			

<210> 453
 <211> 550
 <212> DNA
 <213> Homo sapiens

<400> 453
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 tgggggtgaga gcacagagga gtggggccggg accatgcggg ggacgcggct 100
 ggcgctcctg gcgctggtgc tggctgcctg cggagagctg gcgccggccc 150
 tgcgctgcta cgtctgtccg gagccacag gagtgtcgga ctgtgtcacc 200
 atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250
 ccgggagata gtgtaccctc tccaggggga ctccacggtg accaagtcct 300
 gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350
 cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgccccg 400
 tctgaacagc ctccactgcg gggccctcac gctcctcca ctcttgagcc 450
 tccgactgta gagtccccgc ccacccccat ggccctatgc ggcccagccc 500
 cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaa aaaaaaaaaa 550

<210> 454
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 454

Met	Arg	Gly	Thr	Arg	Leu	Ala	Leu	Leu	Ala	Leu	Val	Leu	Ala	Ala
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Cys	Gly	Glu	Leu	Ala	Pro	Ala	Leu	Arg	Cys	Tyr	Val	Cys	Pro	Glu
				20					25					30
Pro	Thr	Gly	Val	Ser	Asp	Cys	Val	Thr	Ile	Ala	Thr	Cys	Thr	Thr
				35					40					45
Asn	Glu	Thr	Met	Cys	Lys	Thr	Thr	Leu	Tyr	Ser	Arg	Glu	Ile	Val
				50					55					60
Tyr	Pro	Phe	Gln	Gly	Asp	Ser	Thr	Val	Thr	Lys	Ser	Cys	Ala	Ser
				65					70					75
Lys	Cys	Lys	Pro	Ser	Asp	Val	Asp	Gly	Ile	Gly	Gln	Thr	Leu	Pro
				80					85					90
Val	Ser	Cys	Cys	Asn	Thr	Glu	Leu	Cys	Asn	Val	Asp	Gly	Ala	Pro
				95					100					105
Ala	Leu	Asn	Ser	Leu	His	Cys	Gly	Ala	Leu	Thr	Leu	Leu	Pro	Leu
				110					115					120
Leu	Ser	Leu	Arg	Leu										
				125										

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

ctgcagtcag gactctggga ccgcaggggg ctcccggacc ctgactctgc 50

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attttctctt tctttctccc tcttgagtcc ttctgagatg atggctctgg 150

gcgcagcggg agctacccgg gtctttgtcg cgatggtagc ggcggctctc 200

ggcggccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250

ttccaacgct atcaagaacc tgccccacc gctgggcggc gctgcggggc 300

accagggctc tgcagtcagc gccgcgccgg gaatcctgta cccgggcggg 350

aataagtacc agaccattga caactaccag ccgtacccgt gcgcagagga 400

cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450

acgcaggcgt gcaaattctgt ctcgcctgca ggaagcgccg aaaacgctgc 500

atgcgtcacg ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550

tgtgtcttct gatcaaaaatc atttccgagg agaaattgag gaaaccatca 600

ctgaaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650
 accaccttgt cttcaaaaat gtatcacacc aaaggacaag aaggttctgt 700
 ttgtctccgg tcatcagact gtgcctcagg attgtgttgt gctagacact 750
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 aagcatagga gaaaaggctc tcatgggacta gaaatattcc agcgttggtta 850
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 gtaattcttc taggcttcac acttgtcaga gacactaaac cagctatcca 950
 aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000
 ccttcaccaa ctcaatccta aggatataca agttctgtgg ttccagttaa 1050
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 ggtgtgtcac tgcctatttt tctcttctgt atgtaaaattt ttgtacacat 1250
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 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450
 ttaaattata tttcccttta ggctgtgata gtttttgaaa taaaatttaa 1500
 catttaaaaa aaaaaaaaa 1518

<210> 456
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 456
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 20 25 30
 Ala Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu
 35 40 45
 Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val
 50 55 60
 Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln
 65 70 75

Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
				80					85					90	
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
				95					100					105	
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	
				110					115					120	
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	
				125					130					135	
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	
				140					145					150	
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
				155					160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
				170					175					180	
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
				185					190					195	
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	
				200					205					210	
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
				215					220					225	
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
				230					235					240	
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	
				245					250					255	
Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His					
				260					265						

<210> 457
 <211> 638
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,
 509, 556
 <223> unknown base

<400> 457
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 ttttgcagcg gaacgggaag gttttgtggg acccaggttg aaatgacggt 100
 catttttttt tctttctcct tcnngagtcc ttntgagang atggtttttg 150
 gcgcagcggg agctaaccog gttttttgtn gcgatggtag cggcgggtttt 200

cggcggccac cttntgctgg gagtgagcgc caccttgaat cggttttcaa 250
 ttccaacgnt atcaagaacc tgccccacc gntgggcggc gctgcggggc 300
 acccaggntt tgcagtcagc gccgcgccgg gaatcctgta cccgggcggg 350
 aataagtacc agaccattga caattaccag ccgtacccgt gcgcagagga 400
 cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450
 angcgggcgt gcaaantgt ntngcctgca ggaagcgccg aaaacgctgc 500
 atgcgtcang ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550
 tgtgtnttct gatcaaaaatc atttccgagg agaaattgag gaaaccatca 600
 ctgaaagctt tggtaatgat catagcacct tggatggg 638

<210> 458
 <211> 4040
 <212> DNA
 <213> Homo sapiens

<400> 458
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 ttctctctg cacgcggtgc ttgggctcgg ccaggcgggg tccgccgcca 150
 gggtttgagg atgggggagt agctacagga agcgaccccg cgatggcaag 200
 gtatatTTTT gtggaatgaa aaggaaagtat tagaaatgag ctgaagacca 250
 ttcacagatt aatatTTTT gggacagatt tgtgatgctt gattcaccct 300
 tgaagtaatg tagacagaag ttctcaaatt tgcataattac atcaactgga 350
 accagcagtg aatcttaatg ttcacttaaa tcagaacttg cataagaaag 400
 agaatgggag tctgggttaa taaagatgac tatatcagag acttgaaaag 450
 gatcattctc tgttttctga tagtgtatat ggccatttta gtgggcacag 500
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 gaaataagac aagctttcaa gaaattggca ttgaagttac atcctgataa 600
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 ggagaaaagg gacttgagga taatcaaggt ggccagtatg aaagctggaa 750
 ctattatcgt tatgattttg gtatttatga tgatgatcct gaaatcataa 800
 cattggaaag aagagaattt gatgctgctg ttaattctgg agaactgtgg 850

tttgtaaatt tttactcccc aggctgttca cactgccatg atttagctcc 900
 cacatggaga gactttgcta aagaagtgga tgggttactt cgaattggag 950
 ctgttaactg tggatgatgat agaatgcttt gccgaatgaa aggagtcaac 1000
 agctatccca gtctcttcat ttttcggtct ggaatggccc cagtgaataa 1050
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 ttagaagtac agtgacagaa ctttggacag gaaattttgt caactccata 1150
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 aatcttccag attttgaact actttcggca aacacactag aggatcgttt 1350
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 caagtatata aatctaggaa agggatcttc tagtttctgt gttgtttaga 3900
 ctcaaagaat cacaaatttg tcagtaacat gtagttgttt agttataatt 3950
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<210> 459
 <211> 747
 <212> PRT
 <213> Homo sapiens

<400> 459
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 20 25 30
 Gly Thr Asp Gln Asp Phe Tyr Ser Leu Leu Gly Val Ser Lys Thr
 35 40 45
 Ala Ser Ser Arg Glu Ile Arg Gln Ala Phe Lys Lys Leu Ala Leu
 50 55 60
 Lys Leu His Pro Asp Lys Asn Pro Asn Asn Pro Asn Ala His Gly
 65 70 75
 Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu
 80 85 90
 Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu
 95 100 105
 Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr
 110 115 120
 Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu
 125 130 135
 Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe
 140 145 150
 Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala
 155 160 165
 Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg
 170 175 180
 Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met
 185 190 195
 Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly

09978187 101501
TOSTOT 282660

	200	205	210
Met Ala Pro Val	Lys Tyr His Gly Asp 215	Arg Ser Lys Glu Ser 220	Leu 225
Val Ser Phe Ala	Met Gln His Val Arg 230	Ser Thr Val Thr Glu 235	Leu 240
Trp Thr Gly Asn	Phe Val Asn Ser Ile 245	Gln Thr Ala Phe Ala 250	Ala 255
Gly Ile Gly Trp	Leu Ile Thr Phe Cys 260	Ser Lys Gly Gly Asp 265	Cys 270
Leu Thr Ser Gln	Thr Arg Leu Arg Leu 275	Ser Gly Met Leu Phe 280	Leu 285
Asn Ser Leu Asp	Ala Lys Glu Ile Tyr 290	Leu Glu Val Ile His 295	Asn 300
Leu Pro Asp Phe	Glu Leu Leu Ser Ala 305	Asn Thr Leu Glu Asp 310	Arg 315
Leu Ala His His	Arg Trp Leu Leu Phe 320	Phe His Phe Gly Lys 325	Asn 330
Glu Asn Ser Asn	Asp Pro Glu Leu Lys 335	Lys Leu Lys Thr Leu 340	Leu 345
Lys Asn Asp His	Ile Gln Val Gly Arg 350	Phe Asp Cys Ser Ser 355	Ala 360
Pro Asp Ile Cys	Ser Asn Leu Tyr Val 365	Phe Gln Pro Ser Leu 370	Ala 375
Val Phe Lys Gly	Gln Gly Thr Lys Glu 380	Tyr Glu Ile His His 385	Gly 390
Lys Lys Ile Leu	Tyr Asp Ile Leu Ala 395	Phe Ala Lys Glu Ser 400	Val 405
Asn Ser His Val	Thr Thr Leu Gly Pro 410	Gln Asn Phe Pro Ala 415	Asn 420
Asp Lys Glu Pro	Trp Leu Val Asp Phe 425	Phe Ala Pro Trp Cys 430	Pro 435
Pro Cys Arg Ala	Leu Leu Pro Glu Leu 440	Arg Arg Ala Ser Asn 445	Leu 450
Leu Tyr Gly Gln	Leu Lys Phe Gly Thr 455	Leu Asp Cys Thr Val 460	His 465
Glu Gly Leu Cys	Asn Met Tyr Asn Ile 470	Gln Ala Tyr Pro Thr 475	Thr 480
Val Val Phe Asn	Gln Ser Asn Ile His 485	Glu Tyr Glu Gly His 490	His 495

Ser	Ala	Glu	Gln	Ile	Leu	Glu	Phe	Ile	Glu	Asp	Leu	Met	Asn	Pro
				500					505					510
Ser	Val	Val	Ser	Leu	Thr	Pro	Thr	Thr	Phe	Asn	Glu	Leu	Val	Thr
				515					520					525
Gln	Arg	Lys	His	Asn	Glu	Val	Trp	Met	Val	Asp	Phe	Tyr	Ser	Pro
				530					535					540
Trp	Cys	His	Pro	Cys	Gln	Val	Leu	Met	Pro	Glu	Trp	Lys	Arg	Met
				545					550					555
Ala	Arg	Thr	Leu	Thr	Gly	Leu	Ile	Asn	Val	Gly	Ser	Ile	Asp	Cys
				560					565					570
Gln	Gln	Tyr	His	Ser	Phe	Cys	Ala	Gln	Glu	Asn	Val	Gln	Arg	Tyr
				575					580					585
Pro	Glu	Ile	Arg	Phe	Phe	Pro	Pro	Lys	Ser	Asn	Lys	Ala	Tyr	Gln
				590					595					600
Tyr	His	Ser	Tyr	Asn	Gly	Trp	Asn	Arg	Asp	Ala	Tyr	Ser	Leu	Arg
				605					610					615
Ile	Trp	Gly	Leu	Gly	Phe	Leu	Pro	Gln	Val	Ser	Thr	Asp	Leu	Thr
				620					625					630
Pro	Gln	Thr	Phe	Ser	Glu	Lys	Val	Leu	Gln	Gly	Lys	Asn	His	Trp
				635					640					645
Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe
				650					655					660
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val
				665					670					675
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln
				680					685					690
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr
				695					700					705
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg
				710					715					720
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr
				725					730					735
Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu			
				740					745					

<210> 460

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460
actccccagg ctgttcacac tgcc 24

<210> 461
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 461
gatcagccag ccaataccag cagc 24

<210> 462
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 462
gtggtgatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463
<211> 1818
<212> DNA
<213> Homo sapiens

<400> 463
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caccatcatc tactoctact tggagtcgtt ggtgaagttt ttcattcctc 150
agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200
catggaatag gcaggcagac tacttatgaa tttgcaaaac gacagagcat 250
attggttctg tgggatatta ataagcgcg tgtggaggaa actgcagctg 300
agtgccgaaa actaggcgctc actgcgcatg cgtatgtggt agactgcagc 350
aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400
tgatgtaaca atcgtggtga ataatgctgg gacagtatat ccagccgata 450
ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500
ctaggacatt tttggatcac aaaagcactt cttocatoga tgatggagag 550
aaatcatggc cacatogtca cagtggcttc agtgtgcggc cacgaaggga 600
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cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700

aacctcatgt ctctgcccag tttttgtgaa tactggggttc accaaaaaatc 750
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 ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta 850
 tatcaatatac tttctgagac tacagaagtt tcttcctgaa cgcgccctcag 900
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 aaaatcaaaa tgaaatgaat aaataagctc cagccagaga tgtatgcatg 1000
 ataatgatata gaatagtttc gaatcaatgc tgcaaagctt tatttcacat 1050
 tttttcagtc ctgataatat taaaaacatt ggtttggcac tagcagcagt 1100
 caaacgaaca agattaatta cctgtcttcc tgtttctcaa gaatatattac 1150
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 cttattttaca cagggaaggt ttaagactgt tcaagtagca ttccaatctg 1350
 tagccatgcc acagaatatac aacaagaaca cagaatgagt gcacagctaa 1400
 gagatcaagt ttcagcaggc agcttttatct caacctggac atatttttaag 1450
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 aactctgaag tccacaaaaa gtggaccctc tatatttctc ccctttttat 1600
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 gaatttttaag ttctagcccc atgataacct ttttctttgt aatttatgct 1700
 ttcatatatac cttgggtccca gagatgttta gacaatttta ggctcaaaaa 1750
 ttaaagctaa cacaggaaaa ggaactgtac tggctattac ataagaaaca 1800
 atggacccaa gagaagaa 1818

<210> 464

<211> 300

<212> PRT

<213> Homo sapiens

<400> 464

Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Ile Thr Ile Ile
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Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg
 20 25 30

Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	
				35					40					45	
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	
				50					55					60	
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	
				65					70					75	
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	
				80					85					90	
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn	
				95					100					105	
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	
				110					115					120	
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	
				125					130					135	
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	
				140					145					150	
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly	
				155					160					165	
His	Ile	Val	Thr	Val	Ala	Ser	Val	Cys	Gly	His	Glu	Gly	Ile	Pro	
				170					175					180	
Tyr	Leu	Ile	Pro	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe	
				185					190					195	
His	Arg	Gly	Leu	Thr	Ser	Glu	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Gly	
				200					205					210	
Ile	Lys	Thr	Ser	Cys	Leu	Cys	Pro	Val	Phe	Val	Asn	Thr	Gly	Phe	
				215					220					225	
Thr	Lys	Asn	Pro	Ser	Thr	Arg	Leu	Trp	Pro	Val	Leu	Glu	Thr	Asp	
				230					235					240	
Glu	Val	Val	Arg	Ser	Leu	Ile	Asp	Gly	Ile	Leu	Thr	Asn	Lys	Lys	
				245					250					255	
Met	Ile	Phe	Val	Pro	Ser	Tyr	Ile	Asn	Ile	Phe	Leu	Arg	Leu	Gln	
				260					265					270	
Lys	Phe	Leu	Pro	Glu	Arg	Ala	Ser	Ala	Ile	Leu	Asn	Arg	Met	Gln	
				275					280					285	
Asn	Ile	Gln	Phe	Glu	Ala	Val	Val	Gly	His	Lys	Ile	Lys	Met	Lys	
				290					295					300	

<210> 465
 <211> 1547
 <212> DNA
 <213> Homo sapiens

<400> 465

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gagagggccc agcccggccg gggcaggatg accaaggccc ggctgttccg 150
gctgtggctg gtgctggggt cgggtgttcat gatcctgctg atcatcgtgt 200
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gcgcgacgcc cggcgagcc cagaccaggg ccggcagcag gcggagcgga 500
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cgaaaacctc ctccgagact gaaagctttc gcgttgcttt ttctcgctg 1400
cctggaacct gacgcacgcg cactccagtt ttttatgac ctacgatttt 1450

gcaatctggg cttcttggtc actccactgc ctctatccat tgagtactgt 1500

atcgatatgg ttttttaaga ttaatatatt tcaggtatgt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met Thr Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser
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Val Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly
20 25 30

Ala Ala His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr
35 40 45

Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu
50 55 60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser
65 70 75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln
80 85 90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp
95 100 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln
110 115 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser
125 130 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro
140 145 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala
155 160 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg
170 175 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro
185 190 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala
200 205 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys
215 220 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys
230 235 240

Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe	
				245					250					255	
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe	
				260					265					270	
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro	
				275					280					285	
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe	
				290					295					300	
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu	
				305					310					315	
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His	
				320					325					330	
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu	
				335					340					345	
Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg	
				350					355					360	
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser	
				365					370					375	
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln	
				380					385					390	
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr	
				395					400					405	
Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp							
				410											

<210> 467
 <211> 1071
 <212> DNA
 <213> Homo sapiens

<400> 467
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 acgggatggc tacgggaacg cgctatgccg ggaaggtggt ggctcgtgacc 150
 gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200
 cggggcccga gtggttatct gcgacaagga tgagtctggg ggccggggccc 250
 tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300
 gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttggccg 350
 cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400

ctgaggagac ctctgcccag ggattccgcc agctgctgga gctgaaccta 450
ctggggacgt acaccttgac caagctcgcc ctcccctacc tgcggaagag 500
tcaaggggaat gtcacaaaca tctccagcct ggtgggggca atcggccagg 550
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aaagcttttg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650
ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700
tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750
ggccgcatgg gccagcccgc tgaggtcggg gctgcggcag tgttcctggc 800
ctccgaagcc aacttctgca cgggcattga actgctcgtg acgggggggtg 850
cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900
cccgatatcc cttcctgatt tctctcattt ctacttgggg ccccttcct 950
aggactctcc caccctaaac tccaacctgt atcagatgca gcccctaac 1000
ccttagactc taagcccagt tagcaagggt cggggtcacc ctgcagggtc 1050
ccataaaaac gatttgcagc c 1071

<210> 468

<211> 270

<212> PRT

<213> Homo sapiens

<400> 468

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Gly	Gly	Gly	Arg	Gly	Ile	Gly	Ala	Gly	Ile	Val	Arg	Ala	Phe	Val
				20					25					30

Asn	Ser	Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly
				35					40					45

Gly	Arg	Ala	Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu
				50					55					60

Cys	Asp	Val	Thr	Gln	Glu	Asp	Asp	Val	Lys	Thr	Leu	Val	Ser	Glu
				65					70					75

Thr	Ile	Arg	Arg	Phe	Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala
				80					85					90

Gly	His	His	Pro	Pro	Pro	Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln
				95					100					105

Gly	Phe	Arg	Gln	Leu	Leu	Glu	Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr
				110					115					120

Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn	
				125					130					135	
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln	
				140					145					150	
Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr	
				155					160					165	
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn	
				170					175					180	
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu	
				185					190					195	
Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met	
				200					205					210	
Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly	
				215					220					225	
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly	
				230					235					240	
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys	
				245					250					255	
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser	
				260					265					270	

<210> 469
 <211> 687
 <212> DNA
 <213> Homo sapiens

<400> 469
 aggcgggcag cagctgcagg ctgaccttgc agcttggcgg aatggactgg 50
 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100
 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150
 ccttggtccc tggccctcac caggtgccac tggacctggt gtcacggatg 200
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300
 acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400
 gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450
 gcatggtgag cgtgccggtg ttcagccagg ttcctgtgcg ccgccgcctc 500
 tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550

gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600
gccaggccag cagcccagaga ccatactcct tgcacctttg tgccaagaaa 650
ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470
<211> 180
<212> PRT
<213> Homo sapiens

<400> 470
Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile
1 5 10 15
Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
20 25 30
Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val
35 40 45
Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu
50 55 60
Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn
65 70 75
Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu
80 85 90
Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile
95 100 105
Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg
110 115 120
Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp
125 130 135
Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
140 145 150
Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln
155 160 165
Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
170 175 180

<210> 471
<211> 2368
<212> DNA
<213> Homo sapiens

<400> 471
gcgcccgcag gcgtaggcgg ggtggccctt gcgtctcccg cttccttgaa 50
aaaccggcg ggcgagcgag gctgcggggc ggccgctgcc cttccccaca 100

ctccccgccg agaagcctcg ctccggcgccc aacatggcgg gtggggcgctg 150
 cggccccgcag ctaacggcgc tcctggccgc ctggatcgcg gctgtggcgg 200
 cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250
 cagcccatga ccgcctccaa ctggacgctg gtgatggagg gcgagtggat 300
 gctgaaatct tacgccccat ggtgtccatc ctgccagcag actgattcag 350
 aatgggaggc ttttgcaaag aatgggtgaaa tacttcagat cagtgtgggg 400
 aaggtagatg tcattcaaga accagggttg agtggccgct tctttgtcac 450
 cactctccca gcattttttc atgcaaagga tgggatattc cgccggtatc 500
 gtggcccagg aatcttcgaa gacctgcaga attatatctt agagaagaaa 550
 tggcaatcag tcgagcctct gactggctgg aaatccccag cttctctaac 600
 gatgtctgga atggctggtc ttttagcat ctctggcaag atatggcatc 650
 ttcacaacta tttcacagtg actcttgaa ttctgcttg gtgttcttat 700
 gtgtttttcg tcatagccac cttggttttt ggccttttta tgggtctggt 750
 cttggtggta atatcagaat gtttctatgt gccacttcca aggcatttat 800
 ctgagcgctt tgagcagaat cgagatcag aggaggctca tagagctgaa 850
 cagttgcagg atgcggagga ggaaaaagat gattcaaag aagaagaaaa 900
 caaagacagc cttgtagatg atgaagaaga gaaagaagat cttggcgatg 950
 aggatgaagc agaggaagaa gaggaggagg acaacttggc tgctgggtgtg 1000
 gatgaggaga gaagtgaggc caatgatcag gggccccag gagaggacgg 1050
 tgtgaccccg gaggaagtag agcctgagga ggctgaagaa ggcattctctg 1100
 agcaaccctg cccagctgac acagagggtg tggaagactc cttgaggcag 1150
 cgtaaaagtc agcatgctga caagggactg tagatttaat gatgcgtttt 1200
 caagaatata caccaaaaaca atatgtcagc ttccctttgg cctgcagttt 1250
 gtaccaaata cttaattttt cctgaatgag caagcttctc ttaaaagatg 1300
 ctctctagtc atttggcttc atggcagtaa gcctcatgta tactaaggag 1350
 agtcttccag gtgtgacaat caggatatag aaaaacaaac gtagtggttg 1400
 gatctgtttg gagactggga tgggaacaag ttcatttact taggggtcag 1450
 agagtctcga ccagaggagg ccattcccag tcctaatacag caccttccag 1500
 agacaaggct gcaggccctg tgaaatgaaa gccaaagcagg agccttggct 1550

cctgagcatc cccaaagtgt aacgtagaag ccttgcaccc ttttcttgtg 1600
 taaagtatatt atttttgtca aattgcagga aacatcaggc accacagtgc 1650
 atgaaaaatc tttcacagct agaaattgaa agggccttgg gtatagagag 1700
 cagctcagaa gtcaccccag ccctctgaat ctctgtgtgt atgtttttatt 1750
 tcttaccttt aatttttcca gcattttccac catgggcatt caggctctcc 1800
 acaactttca ctattatctc ttggtcagag gactccaata acagccagggt 1850
 ttacatgaac tgtgtttgtt cattctgacc taaggggttt agataatcag 1900
 taaccataac ccctgaagct gtgactgcca aacatctcaa atgaaatgtt 1950
 gtggccatca gagactcaaa aggaagtaag gattttacaa gacagattaa 2000
 aaaaaaattg ttttgtccaa aatatagttg ttgttgattt ttttttaagt 2050
 tttctaagca atatttttca agccagaagt cctctaagtc ttgccagtac 2100
 aaggtagtct tgtgaagaaa agttgaatac tgttttgttt tcatctcaag 2150
 gggttccctg ggtcttgaac tactttaata ataactaaaa aaccacttct 2200
 gattttcctt cagtgatgtg cttttggtga aagaattaat gaactccagt 2250
 acctgaaagt gaaagatttg attttggttc catcttctgt aatcttccaa 2300
 agaattatat ctttgtaaatt ctctcaatac tcaatctact gtaagtaccc 2350
 agggaggcta atttcttt 2368

<210> 472
 <211> 349
 <212> PRT
 <213> Homo sapiens

<400> 472
 Met Ala Gly Gly Arg Cys Gly Pro Gln Leu Thr Ala Leu Leu Ala
 1 5 10 15
 Ala Trp Ile Ala Ala Val Ala Ala Thr Ala Gly Pro Glu Glu Ala
 20 25 30
 Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser
 35 40 45
 Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr
 50 55 60
 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu
 65 70 75
 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys
 80 85 90

Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val
				95					100					105
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg
				110					115					120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile
				125					130					135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys
				140					145					150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser
				155					160					165
Ile	Ser	Gly	Lys	Ile	Trp	His	Leu	His	Asn	Tyr	Phe	Thr	Val	Thr
				170					175					180
Leu	Gly	Ile	Pro	Ala	Trp	Cys	Ser	Tyr	Val	Phe	Phe	Val	Ile	Ala
				185					190					195
Thr	Leu	Val	Phe	Gly	Leu	Phe	Met	Gly	Leu	Val	Leu	Val	Val	Ile
				200					205					210
Ser	Glu	Cys	Phe	Tyr	Val	Pro	Leu	Pro	Arg	His	Leu	Ser	Glu	Arg
				215					220					225
Ser	Glu	Gln	Asn	Arg	Arg	Ser	Glu	Glu	Ala	His	Arg	Ala	Glu	Gln
				230					235					240
Leu	Gln	Asp	Ala	Glu	Glu	Glu	Lys	Asp	Asp	Ser	Asn	Glu	Glu	Glu
				245					250					255
Asn	Lys	Asp	Ser	Leu	Val	Asp	Asp	Glu	Glu	Glu	Lys	Glu	Asp	Leu
				260					265					270
Gly	Asp	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu
				275					280					285
Ala	Ala	Gly	Val	Asp	Glu	Glu	Arg	Ser	Glu	Ala	Asn	Asp	Gln	Gly
				290					295					300
Pro	Pro	Gly	Glu	Asp	Gly	Val	Thr	Arg	Glu	Glu	Val	Glu	Pro	Glu
				305					310					315
Glu	Ala	Glu	Glu	Gly	Ile	Ser	Glu	Gln	Pro	Cys	Pro	Ala	Asp	Thr
				320					325					330
Glu	Val	Val	Glu	Asp	Ser	Leu	Arg	Gln	Arg	Lys	Ser	Gln	His	Ala
				335					340					345

Asp Lys Gly Leu

<210> 473
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 473
gtccagccca tgaccgcctc caac 24

<210> 474
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 474
ctctcctcat ccacaccagc agcc 24

<210> 475
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 475
gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476
<211> 2478
<212> DNA
<213> Homo sapiens

<400> 476
atctggttga actacttaag ctttaatttgt taaactccgg taagtaccta 50
gccacatga tttgactcag agattctctt ttgtccacag acagtcattct 100
caggggcaga aagaaaagag ctcccaaag ctatatctat tcaggggctc 150
tcaagaacaa tggaatatca tcctgattta gaaaatttgg atgaagatgg 200
atataactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250
tttcagagaa aggatcgtgt gctgcatctc ctccttggcg cctcattgct 300
gtaatttttg gaatcctatg cttggtaata ctggatgatag ctgtgggcct 350
gggtaccatg ggggttcttt ccagcccttg tcctcctaata tggattatat 400
atgagaagag ctgttatcta ttcagcatgt cactaaattc ctgggatgga 450
agtaaaagac aatgctggca actgggctct aatctcctaa agatagacag 500
ctcaaatgaa ttgggattta tagtaaaaca agtgtcttcc caacctgata 550
attcattttg gataggcctt tctcggtccc agactgaggt accatggctc 600

tgggaggatg gatcaacatt ctcttctaac ttatttcaga tcagaaccac 650
 agctacccaa gaaaacccat ctccaaattg tgtatggatt cacgtgtcag 700
 tcatttatga ccaactgtgt agtgtgccct catatagtat ttgtgagaag 750
 aagttttcaa tgtaagagga aggggtggaga aggagagaga aatatgtgag 800
 gtagtaagga ggacagaaaa cagaacagaa aagagtaaca gctgaggtca 850
 agataaatgc agaaaatggt tagagagctt ggccaactgt aatcttaacc 900
 aagaaattga agggagaggc tgtgatttct gtatttgtcg acctacaggt 950
 aggctagtat tatttttcta gttagtagat ccctagacat ggaatcaggg 1000
 cagccaagct tgagttttta ttttttattt atttattttt ttgagatagg 1050
 gtctcacttt gttaccagg ctggagtga gtggcacaat ctcgactcac 1100
 tgcagctatc totcgcccca gccctcaag tagctgggac tacaggtgca 1150
 tgccaccatg ccaggctaatt ttttggtgtt tttttagag actgggtttt 1200
 gccatgttga ccaagctggt ctctaactcc tgggcttaag tgatctgccc 1250
 gccttgccct cccaaagtgc tgggattaca gatgtgagcc accacacctg 1300
 gccccaaagt tgaattttca ttctgccatt gacttggcat ttacctggg 1350
 taagccataa gcgaatctta atttctggct ctatcagagt tgtttcatgc 1400
 tcaacaatgc cattgaagtg cacggtgtgt tgccacgatt tgaccctcaa 1450
 cttctagcag tatatcagtt atgaactgag ggtgaaatat atttctgaat 1500
 agctaaatga agaaatggga aaaaatcttc accacagtca gagcaatttt 1550
 attattttca tcagtatgat cataattatg attatcatct tagtaaaaag 1600
 caggaaactcc tactttttct ttatcaatta aatagctcag agagtacatc 1650
 tgccatatct ctaatagaat cttttttttt tttttttttt tttgagacag 1700
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 accgcaacct ccgccccctg ggttcaagca attctcctgc ctcagcctcc 1800
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 tttttttagt agagacaggg tttctccatg tcggtcaggg tagtcccgaa 1900
 ctctgacct caagtgatct gcctgcctcg gcctcccaag tgctgggatt 1950
 acaggcgtga gccactgcac ccagcctaga atcttgata atatgtaatt 2000
 gtagggaaac tgctctcata ggaaagtttt ctgcttttta aatacaaaaa 2050

tacataaaaa tacataaaat ctgatgatga atataaaaaa gtaaccaacc 2100
tcattggaac aagtattaac attttggaat atgttttatt agttttgtga 2150
tgtactgttt tacaatTTTT accatTTTTt tcagtaatta ctgtaaaatg 2200
gtattattgg aatgaaacta ttttctctca tgtgtgtgatt tgtcttattt 2250
ttttcataact ttcccactgg tgctatTTTT atttccaatg gatatttctg 2300
tattactagg gaggcattta cagtcctcta atgttgatta atatgtgaaa 2350
agaaattgta ccaattttac taaattatgc agttttaaataa ggatgatttt 2400
atgttatgtg gatttcattt caataaaaaa aaactcttat caaaaaaaaaa 2450
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2478

<210> 477
<211> 201
<212> PRT
<213> Homo sapiens

<400> 477
Met Glu Tyr His Pro Asp Leu Glu Asn Leu Asp Glu Asp Gly Tyr
1 5 10 15
Thr Gln Leu His Phe Asp Ser Gln Ser Asn Thr Arg Ile Ala Val
20 25 30
Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu
35 40 45
Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile
50 55 60
Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro
65 70 75
Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met
80 85 90
Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu
95 100 105
Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe
110 115 120
Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile
125 130 135
Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp
140 145 150
Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala
155 160 165
Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser

	170	175	180
Val Ile Tyr Asp Gln Leu Cys Ser Val	Pro Ser Tyr Ser Ile Cys		
185	190	195	
Glu Lys Lys Phe Ser Met			
200			

<210> 478
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 478
 gtccacagac agtcatctca ggagcag 27

<210> 479
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 479
 acaagtgtct tcccaacctg 20

<210> 480
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 480
 atcctcccag agccatggta cctc 24

<210> 481
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 481
 ccaaggatag ctgttggttc agagaaagga tcgtgtgctg catctcctcc 50

t 51

<210> 482
 <211> 3819
 <212> DNA
 <213> Homo sapiens

<400> 482

ggaaggggag gagcaggcca cacaggcaca ggccggtgag ggacctgccc 50
 agacctggag ggtctcgctc tgtcacacag gctggagtgc agtgggtgtga 100
 tcttggtca tcgtaacctc cacctcccgg gttcaagtga ttctcatgcc 150
 tcagcctccc gagtagctgg gattacaggt ggtgacttcc aagagtgact 200
 ccgtcggagg aaaatgactc cccagtcgct gctgcagacg aactgttcc 250
 tgctgagtct gctcttctg gtccaaggtg cccacggcag gggccacagg 300
 gaagactttc gcttctgcag ccagcggaaac cagacacaca ggagcagcct 350
 ccactacaaa cccacaccag acctgcgcat ctccatcgag aactccgaag 400
 aggccctcac agtccatgcc cctttccctg cagcccaccc tgettcccga 450
 tccttccctg accccagggg cctctaccac ttctgcctct actggaaccg 500
 acatgctggg agattacatc ttctctatgg caagcgtgac ttcttgctga 550
 gtgacaaagc ctctagcctc ctctgcttcc agcaccagga ggagagcctg 600
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 ctcaaggagg cctcggctg ccccgccag ccagcagttg cagagcctgg 850
 agtcgaaact gacctctgtg agattcatgg gggacatggt gtccttcgag 900
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 tggagtactc ggtgctgctg cctcgaacac tcttcagag gacgaaaggc 1050
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 tggggattgt ggtacagaac accaaagtag ccaacctcac ggagcccgtg 1200
 gtgctcactt tccagacca gctacagccg aagaatgtga ctctgcaatg 1250
 tgtgttctgg gttgaagacc ccacattgag cagcccgggg cattggagca 1300
 gtgctgggtg tgagaccgtc aggagagaaa cccaaacatc ctgcttctgc 1350
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 cgccgtgcac aagcactacc tgagcctcct ctctacgtg ggctgtgtcg 1450

tctctgccct ggccctgcctt gtcaccattg ccgcctacct ctgctccagg 1500
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ctgggtgtttc tgttcaacat ggccatgcta gccaccatgg tgggtgcagat 2000
cctgcggctg cgtccccaca cccaaaagtg gtcacatgtg ctgacactgc 2050
tgggcctcag cctggctcctt ggccctgccct gggccttgat cttcttctcc 2100
tttgcttctg gcaccttcca gcttgctgctc ctctaccttt tcagcatcat 2150
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tgcaggcccg ggggtggccc tccctctga agagcaactc agacagcgcc 2250
aggctcccca tcagctcggg cagcacctcg tccagccgca tctaggcctc 2300
cagcccaact gccatgtga tgaagcagag atgaggcctc gtcgcacact 2350
gcctgtggcc cccgagccag gccagcccc aggccagtca gccgcagact 2400
ttggaaagcc caacgaccat ggagagatgg gccgttgcca tgggtggacgg 2450
actcccgggc tgggcttttg aattggcctt ggggactact cggctctcac 2500
tcagctccca cgggactcag aagtgcgccg ccatgctgcc tagggtagctg 2550
tccccacatc tgtcccaacc cagctggagg cctggtctct ccttacaacc 2600
cctgggcccc gccctcattg ctggggggcca ggcccttgat cttgagggtc 2650
tggcacatcc ttaatcctgt gcccctgcct gggacagaaa tgtggctcca 2700
gttgctctgt ctctcgtggg caccctgagg gcactctgca tcctctgtca 2750
ttttaacctc aggtggcacc cagggcgaat gggggccagg gcagaccttc 2800
agggccagag ccctggcgga ggagaggccc tttgccagga gcacagcagc 2850
agctcgcta cctctgagcc caggccccct cctccctca gccccccagt 2900

cctccctcca tcttccctgg ggttctctc ctctcccagg gcctccttgc 2950
 tccttcgttc acagctgggg gtcccccatt ccaatgctgt tttttgggga 3000
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<210> 483
 <211> 693
 <212> PRT
 <213> Homo sapiens

<400> 483
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 20 25 30
 Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser
 35 40 45
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn
 50 55 60
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His
 65 70 75

09978187-101501

Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe	
				80					85					90	
Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	
				95					100					105	
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	
				110					115					120	
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	
				125					130					135	
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	
				140					145					150	
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	
				155					160					165	
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	
				170					175					180	
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	
				185					190					195	
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	
				200					205					210	
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	
				215					220					225	
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	
				230					235					240	
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	
				245					250					255	
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	
				260					265					270	
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	
				275					280					285	
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	
				290					295					300	
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	
				305					310					315	
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	
				320					325					330	
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	
				335					340					345	
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	
				350					355					360	
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	

	365		370		375
Ser Cys Phe Cys	Asn His Leu Thr Tyr	Phe Ala Val Leu Met	Val		
	380	385	390		
Ser Ser Val Glu	Val Asp Ala Val His	Lys His Tyr Leu Ser	Leu		
	395	400	405		
Leu Ser Tyr Val	Gly Cys Val Val Ser	Ala Leu Ala Cys Leu	Val		
	410	415	420		
Thr Ile Ala Ala	Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys	Arg		
	425	430	435		
Arg Lys Pro Arg	Asp Tyr Thr Ile Lys	Val His Met Asn Leu	Leu		
	440	445	450		
Leu Ala Val Phe	Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu	Pro		
	455	460	465		
Val Ala Leu Thr	Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala	Ile		
	470	475	480		
Phe Leu His Phe	Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly	Leu		
	485	490	495		
Glu Gly Tyr Asn	Leu Tyr Arg Leu Val	Val Glu Val Phe Gly	Thr		
	500	505	510		
Tyr Val Pro Gly	Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp	Gly		
	515	520	525		
Phe Pro Ile Phe	Leu Val Thr Leu Val	Ala Leu Val Asp Val	Asp		
	530	535	540		
Asn Tyr Gly Pro	Ile Ile Leu Ala Val	His Arg Thr Pro Glu	Gly		
	545	550	555		
Val Ile Tyr Pro	Ser Met Cys Trp Ile	Arg Asp Ser Leu Val	Ser		
	560	565	570		
Tyr Ile Thr Asn	Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe	Asn		
	575	580	585		
Met Ala Met Leu	Ala Thr Met Val Val	Gln Ile Leu Arg Leu	Arg		
	590	595	600		
Pro His Thr Gln	Lys Trp Ser His Val	Leu Thr Leu Leu Gly	Leu		
	605	610	615		
Ser Leu Val Leu	Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser	Phe		
	620	625	630		
Ala Ser Gly Thr	Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser	Ile		
	635	640	645		
Ile Thr Ser Phe	Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp	Ser		
	650	655	660		

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser
680 685 690

Ser Arg Ile

<210> 484
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 68, 70, 84, 147
<223> unknown base

<400> 484
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ctgccttgca gaggaaancn tcgggactac accntcaagt gcacatgaac 100
ctgctgctgg ccgtcttcct gctggacacg agcttcctgc tcagcgnagc 150
cgggtggccct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200
cctgcacttc tctgtctcac ctgcctttcc tggatgggcc tcgaggggta 250
caacctctac cgactcgtgg tggaggtctt tggcacctat gtccctggct 300
acctactcaa gctgagcgcc atgggctggg gcttcccat ctttctggtg 350
acgctggtgg ccctggtgga tgtggacaac tatggcccca tcattcttggc 400
tgtgcatagg actccagagg gcgtcatcta cccttccatg tgctggatcc 450
gggactccct ggtcagctac atcaccaacc tgggcctctt cagcctggtg 500
tttctgttca acatgg 516

<210> 485
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 485
ggcattggag cagtgtctggg tg 22

<210> 486
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 486
tggaggccta gatgcggctg gacg 24

<210> 487
<211> 2849
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2715
<223> unknown base

<400> 487
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ggttcaggctc cagggttttgc tttgatcctt ttcaaaaaact ggagacacag 100
aagagggctc taggaaaaag ttttgatgg gattatgtgg aaactaccct 150
gcgattctct gctgccagag caggctcggc gcttccaccc cagtgcagcc 200
ttcccctggc ggtggtgaaa gagactcggg agtcgctgct tccaaagtgc 250
ccgccgtgag tgagctctca cccagtcag ccaaatagag ctcttcgggc 300
ttctcctgct gacatctgcc ctggccggcc agagacaggg gactcaggcg 350
gaatccaacc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400
cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450
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gtttgatgaa agatttgggc ttgaagacc agaagatgac atatgcaagt 600
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tggtgtggtt ctggtactgt accaggaaaa cagatttcta aaggaaatca 700
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ccttcagtgc taccoccttc agctttgcca ctggacctgc ttaataatgc 850
tataactgcc tttagtaact tggaagacct tattcgatat cttgaaccag 900
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cagtgtccat aaggggaagaa ctaaagagaa ccgataccat tttctggcca 1100
 ggttgtctcc tgggttaaacg ctgtggtggg aactgtgcct gttgtctcca 1150
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 acgaggtcct tcagttgaga ccaaagaccg gtgtcagggg attgcacaaa 1250
 tcactcaccg acgtggccct ggagcaccat gaggagtgtg actgtgtgtg 1300
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 ccatacctaa tctcagttgt ttgcttcaag gacctttcat cttcaggatt 1450
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 aaaaaaaaaa aaaaaaaaaa aggttttaggg ataacagggt aatgcggcc 2849

<210> 488
 <211> 345
 <212> PRT
 <213> Homo sapiens

<400> 488
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 Gln Arg Gln Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe
 20 25 30
 Gln Phe Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln
 35 40 45
 His Glu Arg Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser
 50 55 60
 Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp
 65 70 75
 Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe
 80 85 90
 Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys
 95 100 105
 Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile Leu
 110 115 120
 Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser
 125 130 135
 Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe
 140 145 150
 Pro Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro
 155 160 165
 Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala
 170 175 180
 Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr
 185 190 195

Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp	Gln	Leu	
				200					205					210	
Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys	
				215					220					225	
Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu	
				230					235					240	
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	
				245					250					255	
Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	
				260					265					270	
Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	
				275					280					285	
Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys	
				290					295					300	
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr	
				305					310					315	
Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu	
				320					325					330	
His	His	Glu	Glu	Cys	Asp	Cys	Val	Cys	Arg	Gly	Ser	Thr	Gly	Gly	
				335					340					345	

<210> 489
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 489
 acttctcagt gtccataagg g 21

<210> 490
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 490
 gaactaaaga gaaccgatac cattttctgg ccaggttgtc 40

<210> 491
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491
caccacagcg tttaaccagg 20

<210> 492
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<223> Synthetic oligonucleotide probe

<400> 492
acaacaggca cagttcccac 20

<210> 493
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 493
ggcggaatcc aacctgagta g 21

<210> 494
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 494
gcggctatcc tcctgtgctc 20

<210> 495
<211> 3283
<212> DNA
<213> Homo sapiens

<400> 495
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gacctctaca ttccattttg gaagaagact aaaaatgggtg tttccaatgt 100
ggacactgaa gagacaaaatt cttatccttt ttaacataat cctaatttcc 150
aaactccttg gggctagatg gtttcctaaa actctgccct gtgatgtcac 200
tctggatgtt ccaaagaacc atgtgatcgt ggactgcaca gacaagcatt 250
tgacagaaat tcctggaggt attcccacga acaccacgaa cctcaccctc 300
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ccatctggta gagatcgatt tcagatgcaa ctgtgtacct attccactgg 400
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 tttagtggac tcacttattt aaaatccctt tacctggatg gaaaccagct 500
 actagagata ccgcagggcc tcccgcctag cttacagctt ctcagccttg 550
 aggccaacaa catcttttcc atcagaaaag agaattctaac agaactggcc 600
 aacatagaaa tactctacct gggccaaaac tggtattatc gaaatccttg 650
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 aatccaagaa gatgatttta ataacctcaa ccaattacaa attcttgacc 850
 taagtggaaa ttgccctcgt tggtataatg ccccatctcc ttgtgcgccg 900
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 ggctctgtgg gagttctgtc cttgagtggc caacaaaccc gcaagctcac 3150
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acaactgcct agtttaccaa ggagaggcct ggc 3283

<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

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Phe Asn Ile Ile Leu Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe
20 25 30

Pro Lys Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn
35 40 45

His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro
50 55 60

Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn
65 70 75

His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His
80 85 90

Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu
95 100 105

Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro
110 115 120

Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp
125 130 135

Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu
140 145 150

Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys
155 160 165

Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly
170 175 180

Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile
185 190 195

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser
200 205 210

Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser
215 220 225

Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile
230 235 240

Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp
245 250 255

Leu	Ser	Gly	Asn	Cys	Pro	Arg	Cys	Tyr	Asn	Ala	Pro	Phe	Pro	Cys	
				260					265					270	
Ala	Pro	Cys	Lys	Asn	Asn	Ser	Pro	Leu	Gln	Ile	Pro	Val	Asn	Ala	
				275					280					285	
Phe	Asp	Ala	Leu	Thr	Glu	Leu	Lys	Val	Leu	Arg	Leu	His	Ser	Asn	
				290					295					300	
Ser	Leu	Gln	His	Val	Pro	Pro	Arg	Trp	Phe	Lys	Asn	Ile	Asn	Lys	
				305					310					315	
Leu	Gln	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Phe	Leu	Ala	Lys	Glu	Ile	
				320					325					330	
Gly	Asp	Ala	Lys	Phe	Leu	His	Phe	Leu	Pro	Ser	Leu	Ile	Gln	Leu	
				335					340					345	
Asp	Leu	Ser	Phe	Asn	Phe	Glu	Leu	Gln	Val	Tyr	Arg	Ala	Ser	Met	
				350					355					360	
Asn	Leu	Ser	Gln	Ala	Phe	Ser	Ser	Leu	Lys	Ser	Leu	Lys	Ile	Leu	
				365					370					375	
Arg	Ile	Arg	Gly	Tyr	Val	Phe	Lys	Glu	Leu	Lys	Ser	Phe	Asn	Leu	
				380					385					390	
Ser	Pro	Leu	His	Asn	Leu	Gln	Asn	Leu	Glu	Val	Leu	Asp	Leu	Gly	
				395					400					405	
Thr	Asn	Phe	Ile	Lys	Ile	Ala	Asn	Leu	Ser	Met	Phe	Lys	Gln	Phe	
				410					415					420	
Lys	Arg	Leu	Lys	Val	Ile	Asp	Leu	Ser	Val	Asn	Lys	Ile	Ser	Pro	
				425					430					435	
Ser	Gly	Asp	Ser	Ser	Glu	Val	Gly	Phe	Cys	Ser	Asn	Ala	Arg	Thr	
				440					445					450	
Ser	Val	Glu	Ser	Tyr	Glu	Pro	Gln	Val	Leu	Glu	Gln	Leu	His	Tyr	
				455					460					465	
Phe	Arg	Tyr	Asp	Lys	Tyr	Ala	Arg	Ser	Cys	Arg	Phe	Lys	Asn	Lys	
				470					475					480	
Glu	Ala	Ser	Phe	Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	
				485					490					495	
Gln	Thr	Leu	Asp	Leu	Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	
				500					505					510	
Ser	Asp	Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	
				515					520					525	
Gly	Asn	Leu	Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	
				530					535					540	
Leu	Ala	Glu	Leu	Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	

545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu	Leu His Lys Leu Glu Val	
560	565	570
Leu Asp Ile Ser Ser Asn Ser His Tyr	Phe Gln Ser Glu Gly Ile	
575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn	Leu Lys Val Leu Gln Lys	
590	595	600
Leu Met Met Asn Asp Asn Asp Ile Ser	Ser Ser Thr Ser Arg Thr	
605	610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu	Glu Phe Arg Gly Asn His	
620	625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp	Asn Arg Tyr Leu Gln Leu	
635	640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu	Leu Asp Ile Ser Lys Asn	
650	655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val	Phe Asp Gly Met Pro Pro	
665	670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys	Asn Gly Leu Lys Ser Phe	
680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys	Asn Leu Glu Thr Leu Asp	
695	700	705
Leu Ser His Asn Gln Leu Thr Thr Val	Pro Glu Arg Leu Ser Asn	
710	715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile	Leu Lys Asn Asn Gln Ile	
725	730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln	Asp Ala Phe Gln Leu Arg	
740	745	750
Tyr Leu Asp Leu Ser Ser Asn Lys Ile	Gln Met Ile Gln Lys Thr	
755	760	765
Ser Phe Pro Glu Asn Val Leu Asn Asn	Leu Lys Met Leu Leu Leu	
770	775	780
His His Asn Arg Phe Leu Cys Thr Cys	Asp Ala Val Trp Phe Val	
785	790	795
Trp Trp Val Asn His Thr Glu Val Thr	Ile Pro Tyr Leu Ala Thr	
800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala	His Lys Gly Gln Ser Val	
815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu	Leu Asp Leu Thr Asn Leu	
830	835	840

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Ile	Leu	Phe	Ser	Leu	Ser	Ile	Ser	Val	Ser	Leu	Phe	Leu	Met	Val	845	850	855
Met	Met	Thr	Ala	Ser	His	Leu	Tyr	Phe	Trp	Asp	Val	Trp	Tyr	Ile	860	865	870
Tyr	His	Phe	Cys	Lys	Ala	Lys	Ile	Lys	Gly	Tyr	Gln	Arg	Leu	Ile	875	880	885
Ser	Pro	Asp	Cys	Cys	Tyr	Asp	Ala	Phe	Ile	Val	Tyr	Asp	Thr	Lys	890	895	900
Asp	Pro	Ala	Val	Thr	Glu	Trp	Val	Leu	Ala	Glu	Leu	Val	Ala	Lys	905	910	915
Leu	Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys	Leu	Glu	Glu	920	925	930
Arg	Asp	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	Ser	Gln	935	940	945
Ser	Ile	Gln	Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Asp	Lys	950	955	960
Tyr	Ala	Lys	Thr	Glu	Asn	Phe	Lys	Ile	Ala	Phe	Tyr	Leu	Ser	His	965	970	975
Gln	Arg	Leu	Met	Asp	Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe	980	985	990
Leu	Glu	Lys	Pro	Phe	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	995	1000	1005
Arg	Leu	Cys	Gly	Ser	Ser	Val	Leu	Glu	Trp	Pro	Thr	Asn	Pro	Gln	1010	1015	1020
Ala	His	Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Ala	Thr	1025	1030	1035
Asp	Asn	His	Val	Ala	Tyr	Ser	Gln	Val	Phe	Lys	Glu	Thr	Val		1040	1045	

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 <211> 4199
 <212> DNA
 <213> Homo sapiens

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 gaagctatcc ttgtgatgag aaaaagcaaa atgactcagt tattgcagag 200
 tgcagcaatc gtcgactaca ggaagttccc caaacggtgg gcaaatatgt 250

gacagaacta gacctgtctg ataatttcat cacacacata acgaatgaat 300
 catttcaagg gctgcaaaat ctactataaa taaatctaaa ccacaacccc 350
 aatgtacagc accagaacgg aaatcccggt atacaatcaa atggcttgaa 400
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 ttgaagacaa ccagttaccc caaataccct ctggtttgcc agagtctttg 500
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 catttcaaga cttataaact tgaaaaatct ctatttggcc tggaactgct 600
 attttaacaa agtttgcgag aaaactaaca tagaagatgg agtatttgaa 650
 acgctgacaa atttggagtt gctatcacta tctttcaatt ctctttcaca 700
 cgtgccaccc aaactgccaa gctccctacg caaacttttt ctgagcaaca 750
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 acattactag atttaagcgg gaactgtccg aggtgcttca atgccccatt 850
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 gctggatctt gaattcaact atttagtggg agaaatagtc tctggggcat 1050
 ttttaacgat gctgccccgc ttagaaatac ttgacttgtc ttttaactat 1100
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 cgttggtaaa agatacccg cagagttatg caaatagttc ctcttttcaa 1400
 cgtcatatcc ggaaacgacg ctcaacagat tttgagtttg acccacattc 1450
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 ctgtaacatt tgacttctaa ggttttagatg ccatttaaga actgagatgg 4050
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 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln Asn Asp Ser Val
 35 40 45
 Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr

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				50					55					60
Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
				65					70					75
Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
				80					85					90
Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
				95					100					105
Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
				110					115					120
Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
				125					130					135
Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
				140					145					150
Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
				155					160					165
Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
				170					175					180
Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
				185					190					195
Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210
Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
				215					220					225
Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235					240
Asp	Phe	Lys	Gly	Leu	Ile	Asn	Leu	Thr	Leu	Leu	Asp	Leu	Ser	Gly
				245					250					255
Asn	Cys	Pro	Arg	Cys	Phe	Asn	Ala	Pro	Phe	Pro	Cys	Val	Pro	Cys
				260					265					270
Asp	Gly	Gly	Ala	Ser	Ile	Asn	Ile	Asp	Arg	Phe	Ala	Phe	Gln	Asn
				275					280					285
Leu	Thr	Gln	Leu	Arg	Tyr	Leu	Asn	Leu	Ser	Ser	Thr	Ser	Leu	Arg
				290					295					300
Lys	Ile	Asn	Ala	Ala	Trp	Phe	Lys	Asn	Met	Pro	His	Leu	Lys	Val
				305					310					315
Leu	Asp	Leu	Glu	Phe	Asn	Tyr	Leu	Val	Gly	Glu	Ile	Val	Ser	Gly
				320					325					330
Ala	Phe	Leu	Thr	Met	Leu	Pro	Arg	Leu	Glu	Ile	Leu	Asp	Leu	Ser
				335					340					345

Phe Asn Tyr Ile	Lys Gly Ser Tyr Pro	Gln His Ile Asn Ile	Ser
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Arg Asn Phe Ser	Lys Leu Leu Ser Leu	Arg Ala Leu His Leu	Arg
365	370	375	
Gly Tyr Val Phe	Gln Glu Leu Arg Glu	Asp Asp Phe Gln Pro	Leu
380	385	390	
Met Gln Leu Pro	Asn Leu Ser Thr Ile	Asn Leu Gly Ile Asn	Phe
395	400	405	
Ile Lys Gln Ile	Asp Phe Lys Leu Phe	Gln Asn Phe Ser Asn	Leu
410	415	420	
Glu Ile Ile Tyr	Leu Ser Glu Asn Arg	Ile Ser Pro Leu Val	Lys
425	430	435	
Asp Thr Arg Gln	Ser Tyr Ala Asn Ser	Ser Ser Phe Gln Arg	His
440	445	450	
Ile Arg Lys Arg	Arg Ser Thr Asp Phe	Glu Phe Asp Pro His	Ser
455	460	465	
Asn Phe Tyr His	Phe Thr Arg Pro Leu	Ile Lys Pro Gln Cys	Ala
470	475	480	
Ala Tyr Gly Lys	Ala Leu Asp Leu Ser	Leu Asn Ser Ile Phe	Phe
485	490	495	
Ile Gly Pro Asn	Gln Phe Glu Asn Leu	Pro Asp Ile Ala Cys	Leu
500	505	510	
Asn Leu Ser Ala	Asn Ser Asn Ala Gln	Val Leu Ser Gly Thr	Glu
515	520	525	
Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr Asn	Asn
530	535	540	
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser	Asp
545	550	555	
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg	Ile
560	565	570	
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr	Asn
575	580	585	
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu	Thr
590	595	600	
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val	Phe
605	610	615	
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn	Arg
620	625	630	
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu	Asp

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Leu Ser Leu Asn Arg Leu Lys His Ile	Pro Asn Glu Ala Phe Leu	
650	655	660
Asn Leu Pro Ala Ser Leu Thr Glu Leu	His Ile Asn Asp Asn Met	
665	670	675
Leu Lys Phe Phe Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg Leu	
680	685	690
Glu Leu Leu Asp Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr Asp	
695	700	705
Ser Leu Ser Asp Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu Ser	
710	715	720
His Asn Arg Ile Ser His Leu Pro Ser	Gly Phe Leu Ser Glu Val	
725	730	735
Ser Ser Leu Lys His Leu Asp Leu Ser	Ser Asn Leu Leu Lys Thr	
740	745	750
Ile Asn Lys Ser Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu Ser	
755	760	765
Met Leu Glu Leu His Gly Asn Pro Phe	Glu Cys Thr Cys Asp Ile	
770	775	780
Gly Asp Phe Arg Arg Trp Met Asp Glu	His Leu Asn Val Lys Ile	
785	790	795
Pro Arg Leu Val Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln Arg	
800	805	810
Gly Lys Ser Ile Val Ser Leu Glu Leu	Thr Thr Cys Val Ser Asp	
815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe	Thr Phe Phe Ile Thr Thr	
830	835	840
Met Val Met Leu Ala Ala Leu Ala His	His Leu Phe Tyr Trp Asp	
845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu	Ala Lys Val Lys Gly Tyr	
860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe	Tyr Asp Ala Tyr Ile Ser	
875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr	Asp Trp Val Ile Asn Glu	
890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg	Asp Lys Asn Val Leu Leu	
905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro	Gly Leu Ala Ile Ile Asp	
920	925	930

Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val
 935 940 945
 Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe
 950 955 960
 Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile
 965 970 975
 Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu
 980 985 990
 Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro
 995 1000 1005
 Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn
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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 503
catccatggt ctcattccatt agcc 24

<210> 504
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 504
tcgacaacct catgcagagc atcaacacaa gcaagaaaac agtatt 46

<210> 505
<211> 1738
<212> DNA
<213> Homo sapiens

<400> 505
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gtgcctccag gcggccagt ggctgaggg cccagcaagg gctaggggtc 200
atctccagtc ccaggacaca gcagcggcca ccatggccac gcctggggtc 250
cagcagcatc agcagcccc aggaccggg aggcacaggt ggccccacc 300
accgggagga gcagctcctg cccctgtccg ggggatgact gattctctc 350
cgccaggcca cccagaggag aaggccacc cgcctggagg cacaggccat 400
gaggggctct caggaggtgc tgctgatgtg gcttctggtg ttggcagtg 450
gcggcacaga gcagcctac cggcccggcc gtaggggtgtg tgctgtccg 500

gtcacgggg accctgtctc cgagtcgttc gtgcagcgtg tgtaccagcc 550
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gccaacttg tttattgcag cttataatgg ttacaaat 1738

<210> 506
<211> 273
<212> PRT
<213> Homo sapiens

<400> 506
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09970187.101501

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Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	
				35					40					45	
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	
				50					55					60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	
				65					70					75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	
				80					85					90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	
				95					100					105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	
				110					115					120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	
				125					130					135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	
				140					145					150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	
				155					160					165	
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	
				170					175					180	
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	
				185					190					195	
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	
				200					205					210	
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	
				215					220					225	
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	
				230					235					240	
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	
				245					250					255	
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	
				260					265					270	

Lys Asp Ser

<210> 507
 <211> 1700
 <212> DNA
 <213> Homo sapiens

<400> 507

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tggcagcaaa gttcagcttg gctgggcccg ctgtgagggg cttcgcgcta 200
cgccctgcgg tgtcccagg gctgaggtct cctcatcttc tccctagcag 250
tggatgagca acccaacggg ggcccgggga ggggaactgg ccccgaggga 300
gaggaacccc aaagccacat ctgtagccag gatgagcagt gtgaatccag 350
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<210> 508
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 508
 Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu
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 Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val
 20 25 30
 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
 35 40 45
 Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
 50 55 60
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
 65 70 75
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
 80 85 90
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
 95 100 105
 Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
 110 115 120
 Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
 125 130 135
 Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln
 140 145 150
 Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu
 155 160 165
 Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly
 170 175 180
 Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala
 185 190 195
 Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu
 200 205 210

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu
				245					250					255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys
				260					265					270

Lys Asp Ser

<210> 509
 <211> 1538
 <212> DNA
 <213> Homo sapiens

<400> 509
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 ctgaggcccc agcaagggct agggctccatc tccagtccca ggacacagca 150
 gcggccacca tggccacgcc tgggctccag cagcatcagc agccccagg 200
 accggggagg cacaggtggc cccaccacc cggaggagca gctcctgccc 250
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 caccctggc tacccccacc ctggctaccc caacggcatc ccaaggccag 1400
 gtggggccctc agctgagga aggtacgagc tccctgctgg agcctgggac 1450
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 ctgctgcctg acccccagca caataaaaat gaaacgtg 1538

<210> 510
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 510
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 20 25 30
 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
 35 40 45
 Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
 50 55 60
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
 65 70 75
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
 80 85 90
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
 95 100 105
 Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
 110 115 120
 Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
 125 130 135
 Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln

	140		145		150
Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu					
	155		160		165
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly					
	170		175		180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala					
	185		190		195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu					
	200		205		210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala					
	215		220		225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu					
	230		235		240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu					
	245		250		255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys					
	260		265		270

Lys Asp Ser

<210> 511
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 511
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<210> 512
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 512
 ttttcactc ctgtcgggtt gg 22

<210> 513
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 513
ggtgacactt gccagtcaga tgtggatgaa tgcaagtcta ggaggg 46

<210> 514
<211> 2690
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2039-2065
<223> unknown base

<400> 514
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agttgggtct ccgtgtttca ggccggctcc cccttcctgg tctcccttct 200
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ccagggtcct gtctggatga cttatgcggt gggggagtgt aaaccggaac 2650
ttttcatcta tttgaaggcg attaaactgt gtctaatagca 2690

<210> 515
<211> 364
<212> PRT
<213> Homo sapiens

<400> 515
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Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met
20 25 30
Met Ala Arg Gln Lys Gly Ile Phe Tyr Leu Thr Leu Phe Leu Ile
35 40 45
Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu
50 55 60
Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu
65 70 75
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp
80 85 90
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile
95 100 105
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln
110 115 120
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile
125 130 135
Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro
140 145 150
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe
155 160 165
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn
170 175 180
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr
185 190 195
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser
200 205 210
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr
215 220 225
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val

230	235	240
Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr		
245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val		
260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu		
275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly		
290	295	300
Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln		
305	310	315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu		
320	325	330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu		
335	340	345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala		
350	355	360
Glu Ala Glu Lys		

<210> 516
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 38, 88, 118, 135, 193, 213, 222
 <223> unknown base

<400> 516
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 tgaattaggt attatagggg tggtgggggtt gatttttntt cctggaggct 100
 tttggctttg gactctcnct ttctcccaca gagcncttcg accatcactg 150
 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200
 tcttcatcct ttntctctcc cncctcacia totatgtctt cgccttcaac 250
 atcgt 255

<210> 517
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 517

caacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

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<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

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 <211> 344
 <212> PRT
 <213> Homo sapiens

<400> 523
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 Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp
 50 55 60
 Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu
 65 70 75
 Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu
 80 85 90
 Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val
 95 100 105
 Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp
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 Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser
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 170 175 180
 Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln
 185 190 195
 Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro
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 Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile
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 Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr

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Leu Gln Cys Glu	Ala Ser Ala Val Pro	Ser Ala Glu Phe Gln	Trp
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Tyr Lys Asp Asp	Lys Arg Leu Ile Glu	Gly Lys Lys Gly Val	Lys
	260	265	270
Val Glu Asn Arg	Pro Phe Leu Ser Lys	Leu Ile Phe Phe Asn	Val
	275	280	285
Ser Glu His Asp	Tyr Gly Asn Tyr Thr	Cys Val Ala Ser Asn	Lys
	290	295	300
Leu Gly His Thr	Asn Ala Ser Ile Met	Leu Phe Gly Pro Gly	Ala
	305	310	315
Val Ser Glu Val	Ser Asn Gly Thr Ser	Arg Arg Ala Gly Cys	Val
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Trp Leu Leu Pro	Leu Leu Val Leu His	Leu Leu Leu Lys Phe	
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<211> 503
<212> DNA
<213> Homo sapiens

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<211> 2602
<212> DNA
<213> Homo sapiens

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<210> 526

<211> 736

<212> PRT

<213> Homo sapiens

<400> 526

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Glu	Leu	Val	Leu	Ala	Gly	Ala	Ser	Leu	Leu	Leu	Ala	Ala	Leu	Leu	
				35					40					45	
Leu	Gly	Cys	Leu	Val	Ala	Leu	Gly	Val	Gln	Tyr	His	Arg	Asp	Pro	
				50					55					60	
Ser	His	Ser	Thr	Cys	Leu	Thr	Glu	Ala	Cys	Ile	Arg	Val	Ala	Gly	
				65					70					75	
Lys	Ile	Leu	Glu	Ser	Leu	Asp	Arg	Gly	Val	Ser	Pro	Cys	Glu	Asp	
				80					85					90	
Phe	Tyr	Gln	Phe	Ser	Cys	Gly	Gly	Trp	Ile	Arg	Arg	Asn	Pro	Leu	
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Pro	Asp	Gly	Arg	Ser	Arg	Trp	Asn	Thr	Phe	Asn	Ser	Leu	Trp	Asp	
				110					115					120	
Gln	Asn	Gln	Ala	Ile	Leu	Lys	His	Leu	Leu	Glu	Asn	Thr	Thr	Phe	
				125					130					135	
Asn	Ser	Ser	Ser	Glu	Ala	Glu	Gln	Lys	Thr	Gln	Arg	Phe	Tyr	Leu	
				140					145					150	
Ser	Cys	Leu	Gln	Val	Glu	Arg	Ile	Glu	Glu	Leu	Gly	Ala	Gln	Pro	
				155					160					165	
Leu	Arg	Asp	Leu	Ile	Glu	Lys	Ile	Gly	Gly	Trp	Asn	Ile	Thr	Gly	
				170					175					180	
Pro	Trp	Asp	Gln	Asp	Asn	Phe	Met	Glu	Val	Leu	Lys	Ala	Val	Ala	
				185					190					195	
Gly	Thr	Tyr	Arg	Ala	Thr	Pro	Phe	Phe	Thr	Val	Tyr	Ile	Ser	Ala	
				200					205					210	
Asp	Ser	Lys	Ser	Ser	Asn	Ser	Asn	Val	Ile	Gln	Val	Asp	Gln	Ser	
				215					220					225	
Gly	Leu	Phe	Leu	Pro	Ser	Arg	Asp	Tyr	Tyr	Leu	Asn	Arg	Thr	Ala	
				230					235					240	
Asn	Glu	Lys	Val	Leu	Thr	Ala	Tyr	Leu	Asp	Tyr	Met	Glu	Glu	Leu	
				245					250					255	
Gly	Met	Leu	Leu	Gly	Gly	Arg	Pro	Thr	Ser	Thr	Arg	Glu	Gln	Met	
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Gln	Gln	Val	Leu	Glu	Leu	Glu	Ile	Gln	Leu	Ala	Asn	Ile	Thr	Val	
				275					280					285	
Pro	Gln	Asp	Gln	Arg	Arg	Asp	Glu	Glu	Lys	Ile	Tyr	His	Lys	Met	
				290					295					300	
Ser	Ile	Ser	Glu	Leu	Gln	Ala	Leu	Ala	Pro	Ser	Met	Asp	Trp	Leu	
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Glu Pro Val Val	Val Tyr Gly Met Asp	Tyr Leu Gln Gln Val	Ser		
	335	340	345		
Glu Leu Ile Asn	Arg Thr Glu Pro Ser	Ile Leu Asn Asn Tyr	Leu		
	350	355	360		
Ile Trp Asn Leu	Val Gln Lys Thr Thr	Ser Ser Leu Asp Arg	Arg		
	365	370	375		
Phe Glu Ser Ala	Gln Glu Lys Leu Leu	Glu Thr Leu Tyr Gly	Thr		
	380	385	390		
Lys Lys Ser Cys	Val Pro Arg Trp Gln	Thr Cys Ile Ser Asn	Thr		
	395	400	405		
Asp Asp Ala Leu	Gly Phe Ala Leu Gly	Ser Leu Phe Val Lys	Ala		
	410	415	420		
Thr Phe Asp Arg	Gln Ser Lys Glu Ile	Ala Glu Gly Met Ile	Ser		
	425	430	435		
Glu Ile Arg Thr	Ala Phe Glu Glu Ala	Leu Gly Gln Leu Val	Trp		
	440	445	450		
Met Asp Glu Lys	Thr Arg Gln Ala Ala	Lys Glu Lys Ala Asp	Ala		
	455	460	465		
Ile Tyr Asp Met	Ile Gly Phe Pro Asp	Phe Ile Leu Glu Pro	Lys		
	470	475	480		
Glu Leu Asp Asp	Val Tyr Asp Gly Tyr	Glu Ile Ser Glu Asp	Ser		
	485	490	495		
Phe Phe Gln Asn	Met Leu Asn Leu Tyr	Asn Phe Ser Ala Lys	Val		
	500	505	510		
Met Ala Asp Gln	Leu Arg Lys Pro Pro	Ser Arg Asp Gln Trp	Ser		
	515	520	525		
Met Thr Pro Gln	Thr Val Asn Ala Tyr	Tyr Leu Pro Thr Lys	Asn		
	530	535	540		
Glu Ile Val Phe	Pro Ala Gly Ile Leu	Gln Ala Pro Phe Tyr	Ala		
	545	550	555		
Arg Asn His Pro	Lys Ala Leu Asn Phe	Gly Gly Ile Gly Val	Val		
	560	565	570		
Met Gly His Glu	Leu Thr His Ala Phe	Asp Asp Gln Gly Arg	Glu		
	575	580	585		
Tyr Asp Lys Glu	Gly Asn Leu Arg Pro	Trp Trp Gln Asn Glu	Ser		
	590	595	600		
Leu Ala Ala Phe	Arg Asn His Thr Ala	Cys Met Glu Glu Gln	Tyr		
	605	610	615		

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Asn	Gln	Tyr	Gln	Val	Asn	Gly	Glu	Arg	Leu	Asn	Gly	Arg	Gln	Thr
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Leu	Gly	Glu	Asn	Ile	Thr	Asp	Asn	Gly	Gly	Leu	Lys	Ala	Ala	Tyr
				635					640					645
Asn	Ala	Tyr	Lys	Ala	Trp	Leu	Arg	Lys	His	Gly	Glu	Glu	Gln	Gln
				650					655					660
Leu	Pro	Ala	Val	Gly	Leu	Thr	Asn	His	Gln	Leu	Phe	Phe	Val	Gly
				665					670					675
Phe	Ala	Gln	Val	Trp	Cys	Ser	Val	Arg	Thr	Pro	Glu	Ser	Ser	His
				680					685					690
Glu	Gly	Leu	Val	Thr	Asp	Pro	His	Ser	Pro	Ala	Arg	Phe	Arg	Val
				695					700					705
Leu	Gly	Thr	Leu	Ser	Asn	Ser	Arg	Asp	Phe	Leu	Arg	His	Phe	Gly
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Cys	Pro	Val	Gly	Ser	Pro	Met	Asn	Pro	Gly	Gln	Leu	Cys	Glu	Val
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Trp

<210> 527
<211> 4308
<212> DNA
<213> Homo sapiens

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<222> 1478, 3978, 4057-4058, 4070
<223> unknown base

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 aaaaacgaat attgcagtgata atgtgtgatt ctttaaggct gcaatacaag 1750
 cattcagttc cctgtttcaa taagagtcaa tccacattta caaagatgca 1800
 tttttttctt ttttgataaa aaagcaaata atattgcctt cagattattt 1850
 cttcaaaata taacacatat ctagattttt ctgcttgcat gatattcagg 1900
 tttcaggaat gagccttgta atataactgg ctgtgcagct ctgcttctct 1950
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 aaaaataaac cagagtgatc aagttaaacc atacactatc tctaagtaac 2100
 gaaggagcta ttggactgta aaaatctctt cctgcactga caatgggggtt 2150
 tgagaatttt gcccacact aactcagttc ttgtgatgag agacaattta 2200
 ataacagtat agtaaatata ccatatgatt tcttttagttg tagctaaatg 2250
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 tgggacgttt gtcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2840

<210> 612
 <211> 352
 <212> PRT
 <213> Homo Sapien

<400> 612
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 Ala Ala Val Leu Leu Ser Leu Cys Cys Leu Leu Pro Ser Cys Leu
 20 25 30
 Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn
 35 40 45
 Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu
 50 55 60
 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile
 65 70 75
 Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser
 80 85 90
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn
 95 100 105
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr
 110 115 120
 Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val
 125 130 135
 Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu
 140 145 150
 Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu
 155 160 165
 Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe
 170 175 180
 Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln
 185 190 195
 Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro
 200 205 210
 Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile
 215 220 225
 Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu

	230		235		240
Ile Arg Cys Glu	Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu Trp			
	245	250			255
Tyr Lys Gly Glu	Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile			
	260	265			270
Ile Gln Asn Phe	Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val			
	275	280			285
Thr Gln Glu His	Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys			
	290	295			300
Leu Gly Thr Thr	Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr			
	305	310			315
Ala Gln Tyr Gly	Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys			
	320	325			330
Trp Tyr Leu Val	Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr			
	335	340			345
Leu Lys Asn Ala	Ile Leu Gln				
	350				

<210> 613
 <211> 1797
 <212> DNA
 <213> Homo Sapien

<400> 613
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 aaataagaaa attctcaagg aggacgagct cttgagttag acccaacaag 150
 ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200
 cccaagagga gaaatggggt gaacttctcc ctagctgtgg tggatcatcta 250
 cctgatcctg ctacccgctg gcgctgggct gctgggtggc caagttctga 300
 atctgcaggc gcggctccgg gtccctggaga tgtatttctc caatgacact 350
 ctggcggtctg aggacagccc gtccctctcc ttgctgcagt cagcacaccc 400
 tggagaacac ctggctcagg gtgcatcgag gctgcaagtc ctgcaggccc 450
 aactcacctg ggtccgcgtc agccatgagc acttgctgca gcgggtagac 500
 aacttcactc agaaccaggg gatgttcaga atcaaagggtg aacaaggcgc 550
 ccagggtctt caaggtcaca agggggccat gggcatgcct ggtgcccctg 600
 gcccgccggg accacctgct gagaaggagg ccaagggggc tatgggacga 650

gatggagcaa caggccccctc gggacccccaa ggcccaccgg gagtcaaggg 700
agaggcgggc ctccaaggac cccaggggtgc tccagggaag caaggagcca 750
ctggcacccc aggacccccaa ggagagaagg gcagcaaagg cgatgggggt 800
ctcattggcc caaaagggga aactggaact aaggagaga aaggagacct 850
gggtctccca ggaagcaaag gggacagggg catgaaagga gatgcagggg 900
tcatggggcc tcctggagcc caggggagta aaggtagctt cgggaggcca 950
ggcccaccag gtttggctgg ttttcctgga gctaaaggag atcaaggaca 1000
acctggactg caggggtgtc cgggccctcc tggtagctg ggacaccag 1050
gtgccaaggg tgagcctggc agtgctggct cccctgggag agcaggactt 1100
ccagggagcc ccgggagtc aggagccaca ggctgaaag gaagcaaagg 1150
ggacacagga cttcaaggac agcaaggaag aaaaggagaa tcaggagtgc 1200
caggccctgc aggtgtgaag ggagaacagg ggagcccagg gctggcaggt 1250
cccaagggag cccctggaca agctggccag aaggagagacc agggagtga 1300
aggatcttct ggggagcaag gagtaaagg agaaaaagg gaaagaggtg 1350
aaaactcagt gtccgtcagg attgtcggca gtagtaaccg aggccgggct 1400
gaagtttact acagtggtag ctgggggaca atttgcgatg acgagtggca 1450
aaattctgat gccattgtct tctgccgat gctgggttac tccaaaggaa 1500
gggccctgta caaagtggga gctggcactg ggagatctg gctggataat 1550
gttcagtgtc ggggcacgga gtagaccctg tggagctgca ccaagaatag 1600
ctggggccat catgactgca gccacgagga ggacgcaggc gtggagtgca 1650
gcgtctgacc cggaaaccct ttcacttctc tgctcccag gtgtcctcgg 1700
gctcatatgt gggaaggcag aggatctctg aggagttccc tggggacaac 1750
tgagcagcct ctggagagg gccattaata aagctcaaca tcattga 1797

<210> 614
<211> 520
<212> PRT
<213> Homo Sapien

<400> 614
Met Arg Asn Lys Lys Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu
1 5 10 15
Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu
20 25 30

105101" 28182660

Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln	185	190	195
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln	200	205	210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln	215	220	225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys	230	235	240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro	245	250	255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met	260	265	270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro	275	280	285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln	290	295	300
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val	305	310	315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro			

320	325	330
Gly Arg Ala Gly Leu Pro Gly Ser Pro	Gly Ser Pro Gly Ala Thr	
335	340	345
Gly Leu Lys Gly Ser Lys Gly Asp Thr	Gly Leu Gln Gly Gln Gln	
350	355	360
Gly Arg Lys Gly Glu Ser Gly Val Pro	Gly Pro Ala Gly Val Lys	
365	370	375
Gly Glu Gln Gly Ser Pro Gly Leu Ala	Gly Pro Lys Gly Ala Pro	
380	385	390
Gly Gln Ala Gly Gln Lys Gly Asp Gln	Gly Val Lys Gly Ser Ser	
395	400	405
Gly Glu Gln Gly Val Lys Gly Glu Lys	Gly Glu Arg Gly Glu Asn	
410	415	420
Ser Val Ser Val Arg Ile Val Gly Ser	Ser Asn Arg Gly Arg Ala	
425	430	435
Glu Val Tyr Tyr Ser Gly Thr Trp Gly	Thr Ile Cys Asp Asp Glu	
440	445	450
Trp Gln Asn Ser Asp Ala Ile Val Phe	Cys Arg Met Leu Gly Tyr	
455	460	465
Ser Lys Gly Arg Ala Leu Tyr Lys Val	Gly Ala Gly Thr Gly Gln	
470	475	480
Ile Trp Leu Asp Asn Val Gln Cys Arg	Gly Thr Glu Ser Thr Leu	
485	490	495
Trp Ser Cys Thr Lys Asn Ser Trp Gly	His His Asp Cys Ser His	
500	505	510
Glu Glu Asp Ala Gly Val Glu Cys Ser	Val	
515	520	

<210> 615
 <211> 647
 <212> DNA
 <213> Homo Sapien

<400> 615
 cccacgcgtc cgaaggcaga caaagggttca tttgttaaaga agctccttcc 50
 agcacctcct ctctttctcct tttgccccaaa ctcacccagt gagtgtgagc 100
 atttaagaag catcctctgc caagacccaaa aggaaagaag aaaaagggcc 150
 aaaagccaaa atgaaactga tgggtacttgt tttcaccatt gggctaactt 200
 tgctgctagg agttcaagcc atgcctgcaa atcgctcttc ttgctacaga 250
 aagatactaa aagatcacao ctgtcacaaac cttccggaag gagtagctga 300

cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350
 gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgcca 400
 aaagacgttt tctttggacc aaagatctct ttcgtgattc cttgcaacaa 450
 tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttccac 500
 aaactgcact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550
 tagagcatag attctataaa ttcttacttg tctaagacaa gtaaactctgt 600
 gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaaa 647

<210> 616
 <211> 98
 <212> PRT
 <213> Homo Sapien

<400> 616
 Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu
 1 5 10 15
 Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg
 20 25 30
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
 35 40 45
 Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp
 50 55 60
 Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu
 65 70 75
 Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser
 80 85 90
 Phe Val Ile Pro Cys Asn Asn Gln
 95

<210> 617
 <211> 2558
 <212> DNA
 <213> Homo Sapien

<400> 617
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 cagcctgcag ggctgataag cgaggcatta gtgagattga gagagacttt 100
 accccgccgt ggtggttga gggcgcgag tagagcagca gcacaggcgc 150
 gggccccggg aggccggctc tgctcgcgcc gagatgtgga atctccttca 200
 cgaaaccgac tcggctgtgg ccaccgcgc cgcggcgcgc tggctgtgcg 250
 ctggggcgct ggtgctggcg ggtggcttct ttctcctcgg cttcctcttc 300

ggggtggttta taaaatcctc caatgaagct actaacatta ctccaaagca 350
 taatatgaaa gcatttttgg atgaattgaa agctgagaac atcaagaagt 400
 tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450
 tttcagcttg caaagcaaatt tcaatcccag tggaaagaat ttggcctgga 500
 ttctgttgag ctagctcatt atgatgtcct gttgtcctac ccaaataaga 550
 ctcatcccaa ctacatctca ataattaatg aagatggaaa tgagattttc 600
 aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcgga 650
 tattgtacca cttttcagtg ctttctctcc tcaaggaatg ccagagggcg 700
 atctagtgtg tgtaaactat gcacgaactg aagacttctt taaattggaa 750
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acctcactgt ggcccagggt cgaggaggga tgggtgttga gctagccaat 1950
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acagaaattg ctccaagtt cagtgcagaga ctccaggact ttgacaaaag 2150
caaccaata gtattaagaa tgatgaatga tcaactcatg tttctggaaa 2200
gagcatttat tgatccatta gggttaccag acaggccttt ttataggcat 2250
gtcatctatg ctccaagcag ccacaacaag tatgcagggg agtcattccc 2300
aggaatttat gatgctctgt ttgatattga aagcaaagtg gacccttcca 2350
aggcctgggg agaagtgaag agacagattt atgttgcagc cttcacagtg 2400
caggcagctg cagagacttt gagtgaagta gcctaagagg attttttaga 2450
gaatccgtat tgaatttgtg tggatgtca ctcagaaaga atcgtaatgg 2500
gtatattgat aaattttaaa attggtatat ttgaaataaa gttgaatatt 2550
atatataa 2558

<210> 618
<211> 750
<212> PRT
<213> Homo Sapien

<400> 618
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Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly
20 25 30
Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
35 40 45
Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
50 55 60
Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His
65 70 75
Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
80 85 90

Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	95	100	105
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	110	115	120
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	125	130	135
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly	140	145	150
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser	155	160	165
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	170	175	180
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn	185	190	195
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	200	205	210
Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val	215	220	225
Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys	230	235	240
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	245	250	255
Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	260	265	270
Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	275	280	285
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	290	295	300
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	305	310	315
Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	320	325	330
Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	335	340	345
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	350	355	360
Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	365	370	375
Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser			

	380		385		390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr	Leu		
	395	400		405	
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala	Ser		
	410	415		420	
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp	Ala		
	425	430		435	
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr	Ile		
	440	445		450	
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val	Asp		
	455	460		465	
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys	Glu		
	470	475		480	
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr	Glu		
	485	490		495	
Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro		
	500	505		510	
Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val Phe	Phe		
	515	520		525	
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn		
	530	535		540	
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val		
	545	550		555	
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe		
	560	565		570	
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe		
	575	580		585	
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr		
	590	595		600	
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser		
	605	610		615	
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe	Asp		
	620	625		630	
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys		
	635	640		645	
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val		
	650	655		660	
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe		
	665	670		675	

Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val
				680					685					690
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe
				695					700					705
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp
				710					715					720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala
				725					730					735
Ala	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala
				740					745					750

<210> 619
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 619
 agatgtgaag gtgcaggtgt gccg 24

<210> 620
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 620
 gaacatcagc gctccccgta attcc 25

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<220>
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